

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2003, 08:26:59 ; Search time 23 Seconds
(without alignments)
674.731 Million cell updates/sec

Title: US-09-991-225-2
Perfect score: 1712
Sequence: 1 MEPNGTFNNSRNCTIENF.....KAKTKCVFPVSWLRKTRV 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	1712	100.0	346	1	CLT2_HUMAN
2	1367.5	79.9	345	1	CLT2_PIG
3	1197	69.9	309	1	CLT2_MOUSE
4	1187	69.3	309	1	Q924t9 rattus norv
5	567.5	33.1	339	1	CLT1_RAT
6	563	32.9	340	1	CLT1_PIG
7	560	32.7	352	1	CLT1_MOUSE
8	559	32.7	337	1	CLT1_HUMAN
9	479	28.0	367	1	GP17_HUMAN
10	470	27.5	382	1	CLT1_MELGA
11	467	27.3	382	1	P2YR_CHICK
12	447	26.1	308	1	P2YR_HUMAN
13	447	26.1	373	1	P2YR_RAT
14	446	26.1	373	1	P2YR_BOVIN
15	442	25.8	373	1	P2YR_MOUSE
16	442	25.8	373	1	P2YR_MOUSE
17	440	25.7	361	1	EB12_HUMAN
18	436	25.5	344	1	P2Y5_HUMAN
19	434	25.4	377	1	P2Y2_HUMAN
20	430	25.1	370	1	P2Y2_HUMAN
21	421.5	24.6	374	1	P2Y2_RAT
22	418.5	24.4	373	1	P2Y2_MOUSE
23	416	24.3	342	1	PAFR_CAVHO
24	409.5	23.9	342	1	PAFR_HUMAN
25	407	23.8	537	1	P2Y8_XENLA
26	405	23.7	355	1	CLT1_MACMU
27	404.5	23.6	420	1	PAFL_XENLA
28	404	23.6	341	1	PAFR_MOUSE
29	400.5	23.4	397	1	PAFR_HUMAN
30	398	23.2	380	1	APJ_HUMAN
31	398	23.2	380	1	APJ_MACMU
32	397	23.2	341	1	PAFR_RAT
33	394.5	23.0	355	1	CKR1_HUMAN

34	391.5	22.9	355	1	CKR1_MOUSE
35	391	22.8	328	1	P2Y6_RAT
36	390	22.8	399	1	PAR2_MOUSE
37	389	22.7	361	1	P2Y4_RAT
38	387	22.6	371	1	CML1_RAT
39	386	22.5	373	1	CML1_HUMAN
40	385.5	22.5	361	1	P2Y4_MOUSE
41	385	22.5	328	1	P2Y3_CHICK
42	384	22.4	377	1	APJ_MOUSE
43	383	22.4	397	1	PAR2_RAT
44	382	22.3	371	1	CML1_MOUSE
45	381.5	22.3	328	1	P2Y3_MELGA

RESULT 1

CLT2_HUMAN					
ID	CLT2_HUMAN	STANDARD;	PRT;	346	AA.
AC	Q9NS75; Q9HCQ2;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Cysteinyl leukotriene receptor 2 (CysLTR2) (PSEC0146) (HG57) (HPN321)				
DE	(hgPCR21).				
GN	CysLTR2 OR CysLT2 OR CysLT2R.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE=20374466; PubMed=10913337;				
RA	Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T.,				
RA	Nishikawa T., Kawai Y., Masuno Y., Isegai T., Suzuki Y., Sugano S.,				
RA	Furuichi K.;				
RT	"The molecular characterization and tissue distribution of the human				
RT	cysteinyl leukotriene CysLTR2 receptor.";				
RL	Biochem. Biophys. Res. Commun. 274:316-322(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20459128; PubMed=10851239;				
RA	Heise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,				
RA	Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,				
RA	Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,				
RA	Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,				
RA	Lynch K.R., Evans J.F.;				
RT	"Characterization of the human cysteinyl leukotriene 2 receptor.";				
RL	J. Biol. Chem. 275:30531-30536(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20545741; PubMed=11093801;				
RA	Notbacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,				
RA	Civelli O.;				
RT	"Molecular cloning and characterization of a second human cysteinyl				
RT	leukotriene receptor: discovery of a subtype selective agonist.";				
RL	Mol. Pharmacol. 58:1601-1608(2000).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RA	Dunn M.;				
RA	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RA	Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;				
RA	"Identification of G protein-coupled receptor genes from the human				
RT	genome sequence.";				
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.				
RN	[6]				
RP	SEQUENCE OF 17-346 FROM N.A.				
RA	Suga H.;				
RT	"Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";				

P51675 mus musculu
Q63371 rattus norv
P55086 mus musculu
O35811 rattus norv
O35786 rattus norv
Q99788 homo sapien
Q91387 mus musculu
Q99907 gallus gall
Q99908 mus musculu
P63645 rattus norv
P97468 mus musculu
O93361 meleagris g

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. Stimulation by BAY u9773, a partial agonist, induces specific contractions of pulmonary veins and might also have an indirect role in the relaxation of the pulmonary vascular endothelium. The rank order of affinities for the leukotrienes is LTC4 = LTD4 > LTE4.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in the heart, placenta, spleen, peripheral blood leukocytes and adrenal gland. In lung, expressed in the interstitial macrophages, and slightly in smooth muscle cells.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL; AB038269; BAB03601.1; -

DR EMBL; AF254664; AAG17281.1; -

DR EMBL; AF279611; AAK69485.1; -

DR EMBL; AL137118; CAC29102.1; -

DR EMBL; AB083603; BAB89316.1; -

DR EMBL; AB041644; BAB16379.1; -

DR Genbank; HGNC:18274; CYSLTR2.

DR MIM; 605666; -

DR GO; GO:0004974; F:leukotriene receptor activity; NAS.

DR GO; GO:0030105; P:anaphylaxis; NAS.

DR InterPro; IPR004071; Cysleuk_receptor.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR01533; CYSLTRCPTR.

DR PRINTS; PR00237; GPCRHHODPSN.

DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; FALSE_NEG.

DR PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 43 63 1 (POTENTIAL).

FT DOMAIN 64 72 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 73 93 2 (POTENTIAL).

FT DOMAIN 94 123 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 124 144 3 (POTENTIAL).

FT DOMAIN 145 153 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 154 174 4 (POTENTIAL).

FT DOMAIN 175 204 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 205 225 5 (POTENTIAL).

FT DOMAIN 226 245 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 246 266 6 (POTENTIAL).

FT DOMAIN 267 286 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 287 307 7 (POTENTIAL).

FT DOMAIN 308 346 CYTOPLASMIC (POTENTIAL).

FT DISULFID 111 187 BY SIMILARITY.

FT CARBOHYD 20 20 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 26 26 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 181 181 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 346 AA; 39635 MW; EB54A42DDCE5EEA CRC64;

Query Match 100.0%; Score 1712; DB 1; Length 346;

Best Local Similarity 100.0%; Pred. NO. 4.9e-99;

Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESPNGTSSNNRNTIENKREFFPIVYLIFPFVGLNGLSIYFLQPKKTSVNVF 60

DB 17 MESPNGTSSNNRNTIENKREFFPIVYLIFPFVGLNGLSIYFLQPKKTSVNVF 76

QY 61 MLNLATSDLLFTSTPRADYLRGNSWIFGDLACRIMSYSLYVMYSSYIFLTVLSVVR 120

|||||

Db 77 MLNLATSDLLFTSTPRADYLRGNSWIFGDLACRIMSYSLYVMYSSYIFLTVLSVVR 136

QY 121 FLAMVHPFLLHVTIRSANWILCGIWIIMASSIMLLDSGSEQNGSVTSCLENLNYKIA 180

Db 137 FLAMVHPFLLHVTIRSANWILCGIWIIMASSIMLLDSGSEQNGSVTSCLENLNYKIA 196

QY 181 KLOPMNVIALVWGCGLPPFTLSICYLLIIRVLKVEVPESGLRVSHRKALTTITIIIF 240

Db 197 KLOPMNVIALVWGCGLPPFTLSICYLLIIRVLKVEVPESGLRVSHRKALTTITIIIF 256

QY 241 FLCPLPVHTLRVHLTWTWKVGLCKDRHLKALVITTLALAAANACFNPLLYYFAGENKDL 300

Db 257 FLCPLPVHTLRVHLTWTWKVGLCKDRHLKALVITTLALAAANACFNPLLYYFAGENKDL 316

QY 301 KSALRKGHPQKATKCVFPVSWLKRKTRV 330

Db 317 KSALRKGHPQKATKCVFPVSWLKRKTRV 346

RESULT 2

CLF2_PIG STANDARD; PRT; 345 AA.

ID CLF2_PIG AC Q95N03;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cysteinyll leukotriene receptor 2 (CysLTR2).

GN CYSLTR2 OR CYSLTR2.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Ramohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T., Ohishi T., Soga T., Matsushime H., Furuichi K.;

RT "Characterization of the cloned rat and porcine cysteinyl leukotriene receptors.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL; AB052662; BAB60817.1; -

DR InterPro; IPR004071; Cysleuk_receptor.

DR InterPro; IPR000276; GPCR_Rhodopsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR01533; CYSLTRCPTR.

DR PRINTS; PR00237; GPCRHHODPSN.

DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; FALSE_NEG.

DR PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 44 64 1 (POTENTIAL).

FT DOMAIN 65 73 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 74 94 2 (POTENTIAL).

FT DOMAIN 95 124 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 125 145 3 (POTENTIAL).

FT DOMAIN 146 154 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 155 175 4 (POTENTIAL).

FT DOMAIN 176 205 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 206 226 5 (POTENTIAL).

FT DOMAIN 227 246 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 247 267 6 (POTENTIAL).
 FT DOMAIN 268 287 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 288 308 7 (POTENTIAL).
 FT DOMAIN 309 345 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 112 188 BY SIMILARITY.
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 345 AA; 39410 MW; 501B1P89B9B95905 CRG64;

Query Match 79.9%; Score 1367.5; DB 1; Length 345;
 Best Local Similarity 79.2%; Pred. No. 7.9e-78;
 Matches 262; Conservative 24; Mismatches 42; Indels 3; Gaps 2;

QY 1 MEPNGTSNNNS-RNCTIENKREFPIVILIIFPGVGLNGLSYVFLQYKSTSVNV 59
 DB 17 MEPNSTIGNSNRSTETENKREFPIVILIIFPGVGLNGLSYVFLQYKSTSVNV 76

QY 60 FMLNLALSDFLSTLTPFRADYLRGSMWIFGDLACKRIMSYSLYNNMYSYIYFLVLSV 119
 DB 77 FMLNLALSDFLSTLTPFRADYLRGSMWIFGDLACKRIMSYSLYNNMYSYIYFLVLSV 136

QY 120 RFLAWHPFLLHWTIRSANTLGGIILIMASSIMLLDSEONGSVTSCLNELYKI 179
 DB 137 RFLATVPFRLHHTSIKNWILCGVWIFIMASSTVLLKNGSEKQNVTLCLNELSKV 196

QY 180 AKLOTMYIALVYGCILLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIILII 239
 DB 197 TKLTMYIALVYGVFLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIILII 256

QY 240 FFLCFLPYHYLRTVHLTTHKVKGLCKDRHLKALVTITLALAAANACFNPLLYFAGENKDR 299
 DB 257 FFLCFLPYHYLRTVHLTTHKVKGLCKDRHLKALVTITLALAAANACFNPLLYFAGENKDR 316

QY 300 LKSALRGHPQAKTKCVPVSVWLKRETV 330
 DB 317 LKSALRGKRPQ--KTRCGFSVCWLKRETV 345

RESULT 3

CLNT2_MOUSE STANDARD; PRT; 309 AA.

AC Q920AL;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE Cysteinyln leukotriene receptor 2 (CysLTR2).

GN CysLTR2 OR CysLTR2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10990;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RX MEDLINE=21601669; PubMed=11591709;

RA Hui Y., Yang G., Galcreski H., Figueroa D.J., Austin C.P.,

RA Copeland N.G., Gilbert D.J., Jenkins N.A., Funk C.D.;

RT "The murine cysteinyl leukotriene 2 (CysLTR2) receptor. cDNA and

RT genomic cloning, alternative splicing, and in vitro

RT characterization.";

RL J. Biol. Chem. 276:47489-47495(2001);

CC -I- FUNCTION: Receptor for cysteinyl leukotrienes. The response is

CC mediated via a G-protein that activates a phosphatidylinositol-

CC calcium second messenger system. The rank order of affinities for

CC the leukotrienes is LTC4 = LTD4 >> LTE4.

CC -I- SUBCELLULAR LOCATION: Integral membrane protein.

CC -I- TISSUE SPECIFICITY: Widely expressed at low levels, with highest

CC expression in the spleen, thymus and adrenal gland, and lower in

CC the kidney, brain and peripheral blood leukocytes.

CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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 CC -----

DR EMBL; AF331658; AAK97354.1; -
 DR MGD; MG1:1917336; Cysltr2.
 DR GO; GO:0001631; F:cysteinyln leukotriene receptor activity; IDA.

DR InterPro; IPR004071; Cysleuk receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tmL1; 1.

DR PRINTS; PR01533; CYSLTRRECPT.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; FALSE_NEG.

DR PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 27 47 1 (POTENTIAL).
 FT DOMAIN 48 56 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 57 77 2 (POTENTIAL).
 FT DOMAIN 78 98 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 99 119 3 (POTENTIAL).
 FT DOMAIN 120 138 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 139 159 4 (POTENTIAL).
 FT DOMAIN 160 187 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 188 208 5 (POTENTIAL).
 FT DOMAIN 209 229 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 230 250 6 (POTENTIAL).
 FT DOMAIN 251 271 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 272 292 7 (POTENTIAL).
 FT DOMAIN 293 309 CYTOPLASMIC (POTENTIAL).

FT DISULFID 95 171 BY SIMILARITY.
 FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 309 AA; 35227 MW; 327B14A6EDDD2A02 CRG64;

Query Match

69.9%; Score 1197; DB 1; Length 309;

Best Local Similarity 72.7%; Pred. No. 2.2e-67;

Matches 224; Conservative 31; Mismatches 53; Indels 0; Gaps 0;

QY 1 MEPNGTSNNNSRNCNTIENKREFPIVILIIFPGVGLNGLSYVFLQYKSTSVNVF 60

DB 1 MEVTGTPSSYSNRCNTIENKREFPIVILIIFPGVGLNGLSYVFLQYKSTSVNVF 60

QY 61 MLNLALSDFLSTLTPFRADYLRGSMWIFGDLACKRIMSYSLYNNMYSYIYFLVLSVVR 120

DB 61 MLNLALSDFLSTLTPFRADYLRGSMWIFGDLACKRIMSYSLYNNMYSYIYFLVLSVVR 120

QY 121 FLAWVHPFRLHHTSIKNWILCGVWIFIMASSTVLLKNGSEKQNVTLCLNELSKVIA 180

DB 121 FLAWVHPFRLHHTSIKNWILCGVWIFIMASSTVLLKNGSEKQNVTLCLNELSKVIA 180

QY 181 KLOTMYIALVYGCILLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIILIIIF 240

DB 181 SLLIMNHIAVAGFLPFTLIVCVLIIRLLAKETPESGPAAHRKALTTIVIAMTTF 240

QY 241 FFLCFLPYHYLRTVHLTTHKVKGLCKDRHLKALVTITLALAAANACFNPLLYFAGENKDR 300

DB 241 LFLCFLPYHALRTLHLVTWDKDSCGVHLKATVITLTMAAANSCFNPLLYFAGENFKARL 300

QY 301 KSAALRGKH 308

DB 301 RAIFSKVH 308

RESULT 4

CLNT2_MOUSE STANDARD; PRT; 309 AA.

ID CLNT2_MOUSE

AC Q924T9;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

[illegible]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN-129/SV;
 RX PubMed=11226226;
 RA Maekawa A., Kanaoka Y., Lam B.K., Austen K.F.;
 RT "Identification in mice of two isoforms of the cysteinyl leukotriene 1
 receptor that result from alternative splicing.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:2256-2261(2001).
 [2]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RN STRAIN-C57BL/6; TISSUE=Trachea;
 RX MEDLINE=21562332; PubMed=11705452;
 RA Martin V., Sawyer N., Stocco R., Unett D., Lerner M.R., Abramovitz M.,
 RA Funk C.D.;
 RT "Molecular cloning and functional characterization of murine
 cysteinyl-leukotriene 1 (CysLT1) receptors.";
 RL Biochem. Pharmacol. 62:1193-1200(2001).
 [3]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Blood;
 RX MEDLINE=21240338; PubMed=11342226;
 RA Mollerup J., Jorgensen S.F., Hougard C., Hoffmann E.K.;
 RT "Identification of a murine cysteinyl leukotriene receptor by
 expression in Xenopus laevis oocytes.";
 RL Biochim. Biophys. Acta 1517:455-459(2001).
 [4]
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=T-cell;
 RA Ogasawara H., Izumi T., Shimizu T.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC
 CC -!- FUNCTION: Receptor for cysteinyl leukotrienes mediating an
 constriction of the microvascular smooth muscle during an
 inflammatory response. This response is mediated via a G-protein
 that activates a phosphatidylinositol-calcium second messenger
 system. The rank order of affinities for the leukotrienes is LTD4
 >> LTE4 = LTC4 >> LTE4.
 CC
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named Isoforms=2;
 CC Name=1; Synonyms=Long;
 CC IsoId=099JA4-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short;
 CC IsoId=099JA4-2; Sequence=VSP_001921;
 CC
 CC -!- TISSUE SPECIFICITY: Widely expressed, with higher expression in
 the lung and skin, intermediate levels in the heart, kidney and
 stomach and lower levels in several other tissues. Isoform 1 is
 the most abundant form in all tested tissues.
 CC
 CC -!- MISCELLANEOUS: MK-571, a selective antagonist, was shown to
 inhibit eosinophilia, bronchial hyperactivity and microvascular
 leakage. Zafirlukast (accolate) and pranlukast (Onon) were also
 shown to be selective antagonists.
 CC
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC -----
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 or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL; AF329272; AAK16715.1; -
 CC EMBL; AF329272; AAK16716.1; -
 CC EMBL; AF205830; AAK15433.1; -
 CC EMBL; AF263370; AAF73047.1; -
 CC EMBL; AB044087; BAA96809.1; -
 CC HSP; P34996; IDD.
 CC MGD; MGI:1926218; Cyslt1.
 CC GO; GO:0005887; C:integral to plasma membrane; IDA.
 CC GO; GO:0004974; F:leukotriene receptor activity; IDA.
 CC InterPro; IPR004071; Cysleuk_receptor;
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR01533; CYSLTR1.
 CC

DR PRINTS; PR00237; GPCRHOPOSN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; FALSE_NEG.
 DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KM Alternative splicing.
 FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 44 64 1 (POTENTIAL).
 FT DOMAIN 65 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 73 93 2 (POTENTIAL).
 FT DOMAIN 94 121 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 122 142 3 (POTENTIAL).
 FT DOMAIN 143 156 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 157 177 4 (POTENTIAL).
 FT DOMAIN 178 208 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 209 229 5 (POTENTIAL).
 FT DOMAIN 230 245 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 246 266 6 (POTENTIAL).
 FT DOMAIN 267 291 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 292 312 7 (POTENTIAL).
 FT DOMAIN 313 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 111 188 BY SIMILARITY.
 FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 13 Missing (in isoform 2).
 FT FTId=VSP_001921.
 FT
 FT CONFLICT 176 176 Y -> D (IN REF. 3).
 FT
 FT SEQUENCE 352 AA; 40715 MW; 5BDC94B3F1CD0CAB CRC64;
 Query Match 32.7%; Score 560; DB 1; Length 352;
 Best Local Similarity 38.5%; Pred. No. 4.1e-28;
 Matches 117; Conservative 69; Mismatches 108; Indels 10; Gaps 6;
 QY 10 NNSRNCITENKREFFIVYLIIFFWGLGSLIVYFLOPKKSVNVFNLNLSDL 69
 DB 26 NNTCHDTIDERNQVYSTMYSVISVGVFPFGLVLIYLTITHEKSAFOVMINIALDL 85
 QY 70 LFTSTIPFRADYILRGSNWIFGLACRIMSYSLVNMYSIYELTVLSYVFLAMVHFR 129
 DB 86 LCVCITPLRVVYVHKGLWFGDFLCRLTYALXVNLVCSIFFFTAMSFRCVAIVFPVQ 145
 QY 130 LHWVSIRSAMLCIGIWI-LIMASSIMLLDSGEQSVTSCELENLYKIAK--LQTMN 186
 DB 146 NINLVYTKARFVCGIWIIFVILTSSPFLMYKSYODEKNNTKCFEPQNNQAKVLIILH 205
 QY 187 YIALVVGCLLFFTSICYLIIIRVLLKVEVPESGLRVSHRKALTTIITLIIFLCFLP 246
 DB 206 YVSLFEGFIIPVLIIVCYTMIITLLKNMKKN-MFSRKAIGMIIVVTAAPLVSEMP 263
 QY 247 YHTLRVHTTW--KVGICXD--RLHKALVITLALANACFNPFIYFAGENFKDLKS 302
 DB 264 YHTQRTIHLHLHSETRPCDSVLRMOKSVITLSLAASNCDFDPLLYFFSGNFRRL-S 322
 QY 303 ALRK 306
 DB 323 TFRK 326
 RESULT 8
 CLT1_HUMAN
 ID CLT1_HUMAN STANDARD; PRT; 337 AA.
 AC Q9Y271; 2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteinyl leukotriene receptor 1 (CysLT1) (Cysteinyl leukotriene D4
 receptor) (LTD4 receptor) (HG55) (HMTWF81).
 GN CYSLT1 OR CYSLT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;


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FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 42 63 1 (POTENTIAL).
FT DOMAIN 64 76 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 77 98 2 (POTENTIAL).
FT DOMAIN 99 115 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 116 136 3 (POTENTIAL).
FT DOMAIN 137 155 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 156 177 4 (POTENTIAL).
FT DOMAIN 178 207 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 208 227 5 (POTENTIAL).
FT DOMAIN 228 254 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 255 274 6 (POTENTIAL).
FT DOMAIN 275 292 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 293 317 7 (POTENTIAL).
FT DOMAIN 318 362 CYTOPLASMIC (POTENTIAL).
FT DISULFID 113 191 BY SIMILARITY.
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 362 AA; 41180 MW; 3E128AB9EB64349C CRC64;

Query Match 27.5%; Score 470; DB 1; Length 362;
Best Local Similarity 31.0%; Pred. No. 1.4e-22;
Matches 99; Conservative 82; Mismatches 112; Indels 26; Gaps 7;

QY 5 GTFNNNSRNCIT--ENFKREPPPIVYLIFFWGLNGLSIYVLPQYKSTSVNFM 62
DB 21 GWAAGNASTKSLKTKGQFYLYPTVYILVITGPGNSVAIWMFVHRMPSGSIYVMF 80
QY 63 NLAISDLFIETLPRADRYLGRSNWIFGDLACRTMSYSLYVNMYSIYVFLVLSVREFL 122
DB 81 NLAIDFIETLPRADRYLGRSNWIFGDLACRTMSYSLYVNMYSIYVFLVLSVREFL 140
QY 123 AMVHPRLLVYTSINSAWILGHIWILIMASSIMLL--DSGEQNGSVTSCL----- 173
DB 141 GVVHPLKSLGRKKNAVYSSLVWALVAVIAPILFSGGVRNKTIT-CYDITADEY 199
QY 174 LNIYKATLOTWNYIALVVGCLPFFTLISICVILLIIRVLKVEVPSGLRVSHKALTTI 233
DB 200 LRSIFVYSCITVFMFCI-----PFVILGCVGLIVKALYIKDLNDSPLR---RKSIVLV 251
QY 234 IITLIIFTCFLPHTLTVHVL-----TTWVGLCKDLRLKALVITLALAAANCFNPL 287
DB 252 IIVLTFAVSYLPHVVKTLNLRALDFQTPQMCFAFNKXVATVQVTRGLASINSCVPI 311
QY 288 LYTAGENFKRLKSLRK 306
DB 312 LYTAGDTFRRLSEATRK 330

RESULT 11
P2YR_CHICK STANDARD; PRT; 362 AA.
AC P34996;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN P2Y1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93285340; PubMed=8508924;
RA Webb T.E., Simon J., Krishek B.J., Bateson A.N., Smart T.G.,
RA King B.F., Burrstock G., Barnard E.A.;
RT "Cloning and functional expression of a brain G-protein-coupled ATP
receptor."

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RL FEBS Lett. 324:219-225(1993).
RN [2]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=97026278; PubMed=8872457;
RA van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;
RT "Modelling the P2Y purinoceptor using rhodopsin as template."
RL Drug Des. Discov. 13:133-140(1995).
CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN
CC INSENSITIVE G-PROTEIN. PROBABLY BELONGING TO THE GQ FAMILY THAT
CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, SPINAL CORD, GASTROINTESTINAL TRACT,
CC SPLEEN AND LEG MUSCLE. IS NOT DETECTED IN THE HEART, LIVER,
CC STOMACH, LUNG AND KIDNEY.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; X73268; CAA51716.1; -.
CC PIR; S33733; S33733.
CC PDB; 1DDO; 11-JUL-96.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
CC PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE; PS00262; G-PROTEIN_RECEPTOR_F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; 3D-structure.
CC DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 42 63 1 (POTENTIAL).
CC DOMAIN 64 76 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 77 98 2 (POTENTIAL).
CC DOMAIN 99 115 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 116 136 3 (POTENTIAL).
CC DOMAIN 137 155 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 156 177 4 (POTENTIAL).
CC DOMAIN 178 207 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 208 227 5 (POTENTIAL).
CC DOMAIN 228 254 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 255 274 6 (POTENTIAL).
CC DOMAIN 275 292 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 293 317 7 (POTENTIAL).
CC DOMAIN 318 362 CYTOPLASMIC (POTENTIAL).
CC DISULFID 113 191 BY SIMILARITY.
CC CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC HELIX 42 69
CC HELIX 77 102
CC HELIX 115 137
CC HELIX 154 178
CC HELIX 205 231
CC HELIX 250 275
CC HELIX 290 305
CC TURN 306 307
CC HELIX 308 320
SQ SEQUENCE 362 AA; 41194 MW; A806C88FB9514761 CRC64;

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Query Match 27.3%; Score 467; DB 1; Length 362;

Best Local Similarity 30.7%; Pred. No. 2.2e-22;

Matches 98; Conservative 83; Mismatches 112; Indels 26; Gaps 7;

QY 5 GTFNNNSRNCIT--ENFKREPPPIVYLIFFWGLNGLSIYVLPQYKSTSVNFM 62

DB 21 GWAAGNASTKSLKTKGQFYLYPTVYILVITGPGNSVAIWMFVHRMPSGSIYVMF 80

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Platelet;
FROSTIE; F550204; G_PROTEIN_RECEP_F1_2; 1.

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KW Blood coagulation.
FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 75 74 1 (POTENTIAL).
FT DOMAIN 75 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 146 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 127 147 3 (POTENTIAL).
FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 188 4 (POTENTIAL).
FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 219 238 5 (POTENTIAL).
FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 285 6 (POTENTIAL).
FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 328 7 (POTENTIAL).
FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.
FT CARBOHYD 11 11 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 138 MISSING (IN REF. 1).
SQ SEQUENCE 373 AA; 42071 MW; 4DC7C68B4145392 CRC64;

Query Match 26.1%; Score 446; DB 1; Length 373;
Best Local Similarity 32.1%; Pred. No. 4.4e-21;
Matches 102; Conservative 79; Mismatches 111; Indels 26; Gaps 10;

QY 6 TFSNNRNC--TIENFKREFPIVLIIFWGLNGLSYVFLQPKKSTSVNFMGLN 63
| : : : | : : : : : | : : : : : | : : : : : | : : : : : |
33 TAAVSSFKALTKGQFYLPVAVILVFIIGLGNVAIWMFVFMKPSGISYMFN 92
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
64 LAISDLFIPTFRADYLRGNSWIFGLDGRIMSYSLYVNMYSSTYFTLVLSVVRFLA 123
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
93 LALADFLVLTUPALIFYFNKNTDIFGDAMCKLQRFTHVNLVLSLFTCTSAHRYSS 152
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
124 MVHFRLLHVTSRNAILGLIIV-ILIMASSIMLDSS--EONGSVTSCLE-----L 174
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
153 VVPLKSLGKLRKNAICISLVMLVIVVAISPILFYSGTVGRKNKIT-CYDTSDEYL 211
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
175 NLXIAKLQPMNYIALVGCILLPFTLSICYLIIIRVLKVPESGLRVSHRKALTTII 234
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
212 RSYIYSKCT----TVAMFC-VPLVLILGCGYGLIVVALIYKDLNSPLR--RKSILVI 263
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
235 ITLIIFLCPFLPHTLVHTT---WKVGLC--KDLRHKALVITTLALAAANCFNPL 288
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
264 IVLAVFAVSYPHVMTNLFARLDQTPAMCAFNDRVYATYQVTRGLASLNSCVDPI 323
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
289 YFAGFNFKDLKSLARK 306
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
324 YFLAGDFRRLSRATRK 341

RESULT 15
P2YR_BOVIN STANDARD; PRG; 373 AA.
AC P48042:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN P2RY1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ortic endothelium;
RA MEDLINE=95352058; PubMed=7626079;
RA Henderson D.J., Elliot D.G., Smith G.M., Webb T.E., Dainty I.A.;
RA "Cloning and characterisation of a bovine P2Y receptor.";

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RL Biochem. Biophys. Res. Commun. 212:648-656(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Corpus callosum;
RX MEDLINE=99064562; PubMed=9848096;
RA Deng G., Matute C., Kumar C.K., Fogarty D.J., Miledi R.;
RT "Cloning and expression of a P2y purinoceptor from the adult bovine
RL corpus callosum.";
RL Neurobiol. Dis. 5:259-270(1998).
CC -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC ATP AND ADP.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X87628; CAA60958.1; -.
DR EMBL; J04041; AAC78275.1; -.
DR HSSP; P34996; 1DDD.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7cml; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00337; G-PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS03462; G-PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 53 74 1 (POTENTIAL).
FT DOMAIN 75 87 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 126 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 127 147 3 (POTENTIAL).
FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 188 4 (POTENTIAL).
FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 219 238 5 (POTENTIAL).
FT TRANSMEM 239 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 285 6 (POTENTIAL).
FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 328 7 (POTENTIAL).
FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.
FT CARBOHYD 11 11 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42287 MW; 9270A7175C0BDA76 CRC64;

Query Match 25.8%; Score 442; DB 1; Length 373;
Best Local Similarity 31.0%; Pred. No. 7.8e-21;
Matches 95; Conservative 78; Mismatches 109; Indels 24; Gaps 7;

QY 16 TIENFKREFPIVLIIFWGLNGLSYVFLQPKKSTSVNFMGLNLSLFIETL 75
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
45 TKTGQFYLPVAVILVFIIGLGNVAIWMFVFMKPSGISYMFNLALADFLVLT 104
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
76 PFRADYLRGNSWIFGLDGRIMSYSLYVNMYSSTYFTLVLSVRLAMVHPRLLHVT 135
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
105 PALIFYFNKNTDIFGDAMCKLQRFTHVNLVLSLFTCTSAHRYSGVYIPKSLGLK 164
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
136 IRSAWILCGIIVILIMASSIMLL---DSGSEONGSVTSCLE-----NLXIAKLQPM 186
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
165 KNAVVISLVWLVVVGISPIFYSGTGIRKNKIT-CYDTSDEFLRSYISKCT-- 221
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
187 YIALVGCILLPFTLSICYLIIIRVLKVEPESGLRVSHRKALTTIIITLIIFLCP 246
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :
222 --TVAMFC-VPLVLILGCGYGLIVVALIYKDLNSPLR---RKSILVIIVLTVFAVSIP 275
| : : : | : : : | : : : | : : : | : : : | : : : | : : : | :

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Db 121 FLATVHPMPHVTSSRSWILCGIIVFIMASSALLVNGQEKDNISCELSPOKFK 180
Qy 181 KLQNTNYIALVVGCLLPFFTLSTCYLLIIRVLLKVEVPESGLRVSHRKALTIITLIIF 240
Db 181 LLLIMNHANAVAGFLPFLTLICVILLIRILKABIPESGPAARHKALTIIVIMTF 240
Qy 241 FLCFLPYHTLTHTVHTKVGICKRHLKALVITLALAAANCFNLLYFAGENKDLR 300
Db 241 LFCFLPYHALTLHLNVTWDCSGDVLHKATVITLMAAANCFNLLYFAGENKDLR 300
Qy 301 KSALRKGH 308
Db 301 RAIFSKVH 308

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RESULT 2

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Q8IV19 PRELIMINARY; PRT; 337 AA.
AC Q8IV19;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=Pancreas;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035750; RAH5750.1; -
KW Hypothetical protein.
SQ SEQUENCE 337 AA; 38486 MW; B9B09CE0FD305245 CRC64;

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Query Match 32.3%; Score 553; DB 4; Length 337;
Best Local Similarity 37.7%; Pred. No. 2.4e-37;
Matches 115; Conservative 71; Mismatches 107; Indels 12; Gaps 7;
Qy 11 NSRNC--TIENKREFFPIVLIIFPWGLVNGLSIYVLOPKKSTSVNFMALNSD 68
Db 10 SSATCHDTDDFRNQVSTLSYMSVGGFGNGFLYVLIKTHKSAQVYTMINLAYD 69
Qy 69 LLFISLTPRADYILRGSNWIFGDLACRIMSYSLVNMYSIYFLVLSVRFAMVHPF 128
Db 70 LLCVCTPLRVVYVHKGIWFGDLRLSTYALVNLKCSIFPTAMSFRCIAIVFPV 129
Qy 129 RLHVTSTRSWILCGIWI-LIMASSIMLDGSEQNGSVTSCELEINLYKIAK--LQTM 185
Db 130 QNINLVTKARFCVCGIWIIVLTSSPFIMARPKQDEKNKTCFFEPDQNTKHVLVL 189
Qy 186 NYIALVVGCLLPFFTLSTCYLLIIRVLLKVEVPESGLRVSHRKALTIITLIIFLCL 245
Db 190 HYSLVFGIIFVLIIVCTIITLILLLKSKKN--LSSHKRAIGMIWVTAFLVGF 247
Qy 246 PYHTLTHTVHT--KVGCLKD--RLHKALVITLALAAANCFNLLYFAGENKDLR 301
Db 248 PYHTLTHTVHT--KVGCLKD--RLHKALVITLALAAANCFNLLYFAGENKDLR 306
Qy 302 SALRK 306
Db 307 STFRK 311

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RESULT 3

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Q96P68 PRELIMINARY; PRT; 337 AA.
AC Q96P68;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

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DE G protein-coupled receptor GPR99 (Putative G-protein coupled receptor)
DE (seven transmembrane helix receptor).
GN GPR80 OR GPCR OR GPR99.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE:21458557; PubMed:11574155;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RA "Discovery and mapping of ten novel G protein-coupled receptor
RT genes.";
RL Gene 275:83-91(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX PubMed:12098360;
RA Wittenberger T., Hallebrand S., Munck A., Kreienkamp H.J.,
RA Schaller H.C., Hampe W.;
RT "GPR99, a new G protein-coupled receptor belonging to a new subgroup
RT of nucleotide receptors.";
RL BMC Genomics 3:17-17(2002).
RN [4]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF411109; AAL26480.1; -
DR EMBL; AB083598; BAB89311.1; -
DR EMBL; AF370886; AAM76912.1; -
DR EMBL; AB065877; BAC06095.1; -
DR Genew; HGNC:4531; GPR80.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 337 AA; 38251 MW; 6814EA0044756CE6 CRC64;

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Query Match 28.5%; Score 487.5; DB 4; Length 337;
Best Local Similarity 34.9%; Pred. No. 5.2e-32;
Matches 111; Conservative 64; Mismatches 114; Indels 29; Gaps 10;
Qy 14 NCTIEN--FKREFPIVLIIFWGLVNG--LSIVF--LOPKKSTSVNFMALNSD 68
Db 23 NCTDENPLKMHVLPVYIGIIFLNGFGPNNAVISTIFKRPWKST--LIMLNACTD 79
Qy 69 LLFISLTPRADYILRGSNWIFGDLACRIMSYSLVNMYSIYFLVLSVRFAMVHPF 128
Db 80 LLYLTSLPFLTHYVAGSNWIFGDMCKFIKFSFHFNLKSYSLFLTCFSIFRCVITHPM 139
Qy 129 RLHVTSTRSWILCGIWIILIMASSI---MLLDSSEQNGS---VMSCELEINLYKIAK 181
Db 140 SCFSIHKTRCAVACAVWIIISLVAVIPMTVITSTNRTNRSACLDLTSDELNTIK--- 196
Qy 182 LQTMNYIALVVGCLLPFFTLSTCYLLIIRVLLKVEVPESGLRVSHRKALTIITLIIF 241
Db 197 --WYNLIITATTCPLVIVITLCYTIITHTHGLQTDSCLE--QKARRITILLALAFY 251
Qy 242 LCFEYHTLTHTVHTTKVGL---CKDLKALVITLALAAANCFNLLYFAGENKFD 298
Db 252 VCFLPFHILRVIRIESRLLSISCSSTENGIEHAYIVSRPLAALNTGILLVYVSDNFQ 311

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Query Match      26.5%; Score 453; DB 13; Length 361;
Best Local Similarity 30.4%; Pred. No. 3.6e-29;
Matches 96; Conservative 80; Mismatches 114; Indels 26; Gaps 8;

QY 8 SNNSNRC--ENFKREFFPIVYLIIFWGLVGLNGLSIYVFLQPKKSTSVNFMNLTA 65
DB 23 SAGNTKSLTKGFGFYLPVAVIIVCITGFSVAINWFIIFHKPWSISVIMENLA 82
QY 66 ISDLFISTLPFRADYLRGSMWIFGLACRIMSYSLVNMYSYIYFLVLSVVRFLAMV 125
DB 83 LADFLYVLSLPALFYIYFNKNTWIFGDCALCKLQRFPHVNLXGSLFSLTCLISVHRXGV 142
QY 126 HPRLLHVTSSRSNWILGIIWLLIMASSIMLL---DSGEQNGSVTSCLE-----LNL 176
DB 143 HPLKSLGRLKKNISYISALVWFIAGISPLFFSGTGIRKNKTIIT-CFTDSSDEYLS 201
QY 177 YFIKALQPMYIALVWGCILPFPFTLSICYLLIIRVILKVEVPESGLRVSHRKALTTIIT 236
DB 202 YFIYGNCTI---TVFGCIPFILLGCGYGLIVVALLYKDMNAPLR--KKSIVLYIV 253
QY 237 LIIFLCPFLPYHLRTVHLTT---WKVGLC--KDLRHKALVITLALAAANACNPNLLY 290
DB 254 LTVFAVSLPFLVHMKNLRLARLDQSPENCFNDRVIATYQVTRGLASLNSCVDPI 313
QY 291 FAGENFKDRKLSALRK 306
DB 314 LAGDTFRKLSRATRK 329

RESULT 7
Q8BMJ5 ID Q8BMJ5 PRELIMINARY; PRT; 373 AA.
AC Q8BMJ5;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE P2Y purinoceptor 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Wesonephros;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK030759; BAC27125.1; -.
SQ SEQUENCE 373 AA; 42228 MW; BA88124B7847287C CRC64;

Query Match      25.5%; Score 436.5; DB 11; Length 344;
Best Local Similarity 32.4%; Pred. No. 7.7e-28;
Matches 100; Conservative 72; Mismatches 114; Indels 23; Gaps 8;

QY 8 SNNSNRC--ENFKREFFPIVYLIIFWGLVGLNGLSIYVFLQPKKSTSVNFMNLTA 67
DB 3 SSNGSQPYDDSKFYLYGCMFSVVFVGLISNCAVYIFICALKVRNETTMINLAMS 62
QY 68 DLLEISTLPFRADYLRGSMWIFGLACRIMSYSLVNMYSYIYFLVLSVVRFLAMV 127
DB 63 DLLEFVFTLPFRI--FYFATRNMPFGDLCKTSVLMFTYNNYSGILFLCISVDRFLAIVP 121
QY 128 FRLHVTSSRSNWILGIIWLLIM---ASSIMLLDSGEQNGSVTSCLENLKYIAKLOT 184
DB 122 FKSXTLTKENAKIVCIAWFTVMGSGAPAVFFQSTHSGNNTSEACFE--NFPATATKT 179
QY 195 -MNYIAL---VVGCLLPFTLSICYLLIIRVILKVEVPESGLRVSHRKALTTIITLIIF 240
DB 180 YLSRVIFIEIVGFIFPLILANTVCSMVLTNLK--EVTLSRKMKNKTVLKMIFVHLVIF 238
QY 241 FLCPVHTLRTVHLTTWKVGLCKDRHLKALV-----ITLALAAANACNPNLLYFA 292
DB 239 CFCFVFN---INLLISLARTQTFVNCVVAAVTWYFPTLCIAYNSCCFPIVYFT 294
QY 293 GENFKDRK 301
DB 295 SDTIQNGIK 303

RESULT 9
Q8BKK1 ID Q8BKK1 PRELIMINARY; PRT; 370 AA.
AC Q8BKK1;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE P2Y purinoceptor 9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK051709; BAC34729.1; -.
SQ SEQUENCE 370 AA; 41956 MW; AB126542343AB6E1 CRC64;

Query Match 24.8%; Score 425; DB 11; Length 370;
Best Local Similarity 31.7%; Pred. No. 7.1e-27;
Matches 103; Conservative 68; Mismatches 134; Indels 20; Gaps 9;

QY 5 GTFNNNSRNCIT-ENFKREFPIVLIIFWGLVGLNGLSIYVFLQPKKSTSVNVFMLN 63
Db 23 GNATNTNT--CIVDSSFYKYNLNGAVYSVWFLGLTNSASLFVCFRKMRSRTAIFIN 80
QY 64 LAISDLFLSTLPFRADYLRGSKWIFGLACRIMSYLYVMYSSIFLTVLSVVRFLA 123
Db 81 LALSDDLFLVCTLPFKI-FYNENRHWPGDPLCKISGTAFLNIGSMFLTCTISVDRLA 139
QY 124 MVHPFRLLHVTIRSANWILCOIWIIMASSIML-LDSGSEONGSVTSCELNLYKIAK- 181
Db 140 IVYFPRSTRIRNRNSAIVCAGWILVNGISASLFSTVNNATTCFEGSKRWKT 199
QY 182 -LQTMNVIALVVGCLLPFTTSCYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIF 240
Db 200 YLSKITIFIEVVGFIIPILINVCSSSVVLTAK-PATLSQIGTNKKKVLKMITVMAVF 258
QY 277 KD-----RLKSALRGHPQKAK 313
Db 319 QKSFYINTHRESLFKXTETPLTPK 343

RESULT 10
O57466 PRELIMINARY; PROT; 374 AA.
AC O57466;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE G protein coupled P2Y nucleotide receptor.
GN TP2Y.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=98086419; PubMed=9415702;
RA Boyer J.L., Waldo G.L., Harden T.K.;
RT "Molecular cloning and expression of an avian G protein-coupled P2Y
RT receptor.";
RL Mol. Pharmacol. 52:928-934(1997).
DR EMBL; AF031897; AAC60339.1; -.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 374 AA; 42594 MW; 849C465722BDD02B CRC64;

Query Match 24.8%; Score 424.5; DB 13; Length 374;

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Best Local Similarity 31.0%; Pred. No. 7.9e-27;
Matches 96; Conservative 77; Mismatches 112; Indels 25; Gaps 9;

QY 18 ENFKREFPIVLIIFWGLVGLNGLSIYVFLQPKKSTSVNVFMLNLAISDLFLSTLP 77
Db 37 EEFKFIPLPSYGVIVVGLPLNSWAMWIVSEMPWNAATTYMFENLAISDLTVVFSLT 96
QY 78 RADYYLRGSKWIFGLACRIMSYLYVMYSSIFLTVLSVVRFLAMVHFRLLHVTSTR 137
Db 97 LVYYADRNNWPGFKVFRFLFYANLYSSILFTCTISVHTYMGICHPIRSLKWKTK 156
QY 138 SAWLIGIITWILI--MASSIMLDSGSEONGSV---TSCLELNLYKIAKLQTMNYIAL 190
Db 157 HARLICVGVWLVVTCILPNIIFVTTSSKDNSTLCHDTTKPEEDHY-----VYSSS 209
QY 191 VVGCL--LFFWLTSCYLLIIRVLKVEVPESGLRV-SHRK-ALTTIITLIIFLCLFLP 246
Db 210 IMALLGFIFLVVVCYCLMAKRLCKRSFSPSPRVPSYKRSIKMIIIVLTVFAICFVP 269
QY 247 YHTLRVHLLTT-WKVGCLCK--DRLHKALVITLALAAANACFNPLLYFAGENEKDRLSA 303
Db 270 FHTRILYTSRYFOADCOTLIINFYKITRELASINCLDPIITFMAGDKTRGR---- 325
QY 304 LRKGHPQKAK 313
Db 326 LRGAARPR 335

RESULT 11
Q8BLG2 PRELIMINARY; PROT; 370 AA.
AC Q8BLG2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P2Y purinoceptor 9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK045289; BAC32299.1; -.
SQ SEQUENCE 370 AA; 41872 MW; 0B4C79FEDFD32050 CRC64;

Query Match 24.6%; Score 421; DB 11; Length 370;
Best Local Similarity 31.4%; Pred. No. 1.5e-26;
Matches 102; Conservative 70; Mismatches 133; Indels 20; Gaps 9;

QY 5 GTFNNNSRNCIT-ENFKREFPIVLIIFWGLVGLNGLSIYVFLQPKKSTSVNVFMLN 63
Db 23 GNATNTNT--CIVDSSFYKYNLNGAVYSVWFLGLTNSASLFVCFRKMRSRTAIFIN 80
QY 64 LAISDLFLSTLPFRADYLRGSKWIFGLACRIMSYLYVMYSSIFLTVLSVVRFLA 123
Db 81 LALSDDLFLVCTLPFKI-FYNENRHWPGDPLCKISGTAFLNIGSMFLTCTISVDRLA 139
QY 124 MVHPFRLLHVTIRSANWILCOIWIIMASSIML-LDSGSEONGSVTSCELNLYKIAK- 181
Db 140 IVYFPRSTRIRNRNSAIVCAGWILVNGISASLFSTVNNATTCFEGSKRWKT 199
QY 182 -LQTMNVIALVVGCLLPFTTSCYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIF 240
Db 200 YLSKITIFIEVVGFIIPILINVCSSSVVLTAK-PATLSQIGTNKKKVLKMITVMAVF 258
QY 241 FLCFLPYHTLRVHLLTWKVGCLCK--DRLHKALV-ITLALAAANACFNPLLYFAGENF 296

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RT Gene.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA He B., Tiemann U., Kavitz W., Weikard R., Laurent P., Schwerin M.,
RA Schmidt P.;
RT "Molecular characterization of bovine platelet-activating factor
RT receptor transcripts and their detection in different tissues of
RT cattle.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF107321; AAF01439.2; -.
DR EMBL; AJ295321; CAC43290.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1.1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1.2; 1.
KW Receptor.
SQ SEQUENCE 342 AA; 39691 MW; 704236205AE937C9 CRC64;

Query Match 23.7%; Score 406.5; DB 6; Length 342;
Best Local Similarity 30.3%; Pred. No. 2.le-25;
Matches 100; Conservative 63; Mismatches 140; Indels 27; Gaps 9;

QY 1 MEPNGTFSNNNSRNCNTIENPKREFPPIVLIIFWGLNGLSIYVF--LQPYKKSTSVN 58
DB 1 MEPNSFRVDS-----EFRTLPFIYSIVFVGLVANSYVLWVFARLYPSKKFNEIK 53
QY 59 VFMLNLAIISDLLFISTLPFRADYILRGSNWIFGDLACRIMSYSLYVNMYSYIFLVLSV 118
DB 54 IFWNLTMADLLFLVLPVLIWVYIYNEGDWILPFLCNVAGCLFFINTYCSVAFVGITY 113
QY 119 VFRLAMVHPFRLHLVTSIRSAWILCGIHWILIMASSIMLLDSGS-----EQNGSVTSC 171
DB 114 NRYQAVAYPIKTAQATTKRGISLSLIWVSIVATASYFLATDSTNLVPMKDGSGNITRC 173
QY 172 LE-LNLYKIAKLQTMNKLALVWGC-LLPFTLSICYLIIIRVLLKVEVPESGLRVSHKA 229
DB 174 FEHYEPYRGPIILVHVETAF---CFELVFELIFYCNLIHTLTQPMKQQRKAGVKRRA 230
QY 230 LTTIITLIIFFLCFLPYHTLRTVHLTWKVGCLKDLRHKAL----VITIALAAANACFN 285
DB 231 LWMVCVLAVFICFVPHVVO-LPWTLAELGY-QTFNHQAINDAHQITLCLLSINCVLDP 288
QY 286 PLIYFAGENFKDLKSLAKRGHPQAKTKC 316
DB 289 FVIYCFLLTKKFKRHLS---EKFYSMRSRKC 316

Search completed: October 8, 2003, 08:30:34
Job time : 102 secs
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RT Gene.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA He B., Tiemann U., Kavitz W., Weikard R., Laurent P., Schwerin M.,
RA Schmidt P.;
RT "Molecular characterization of bovine platelet-activating factor
RT receptor transcripts and their detection in different tissues of
RT cattle.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF107321; AAF01439.2; -.
DR EMBL; AJ295321; CAC43290.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1.1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1.2; 1.
KW Receptor.
SQ SEQUENCE 342 AA; 39691 MW; 704236205AE937C9 CRC64;

Query Match 23.3%; Score 399; DB 11; Length 341;
Best Local Similarity 30.5%; Pred. No. 8.7e-25;
Matches 101; Conservative 66; Mismatches 134; Indels 30; Gaps 10;

QY 1 MEPNGTFSNNNSRNCNTIENPKREFPPIVLIIFWGLNGLSIYVF--LQPYKKSTSVN 58
DB 1 MEHNGSFRVDS-----EFRTLPFIYSIVFVGLVANSYVLWVFANLYPSKKLNEIK 53
QY 59 VFMLNLAIISDLLFISTLPFRADYILRGSNWIFGDLACRIMSYSLYVNMYSYIFLVLSV 118
DB 54 IFWNLTMADLLFLVLPVLIWVYIYNEGDWILPFLCNVAGCLFFINTYCSVAFVGITY 113
QY 119 VFRLAMVHPFRLHLVTSIRSAWILCGIHWILIMASSIMLLDSGS-----EQNGSVTSC 171
DB 114 NRYQAVAYPIKTAQATTKRGISLSLIWVSIVATASYFLATDSTNLVPMKDGSGNITRC 173
QY 172 LE-LNLYKIAKLQTMNKLALVWGC-LLPFTLSICYLIIIRVLLKVEVPESGLRVSHKA 229
DB 174 FEHYEPYRGPIILVHVETAF---CFELVFELIFYCNLIHTLTQPMKQQRKAGVKRRA 230
QY 230 LTTIITLIIFFLCFLPYHTLRTVHLTWKVGCLKDLRHKAL----VITIALAAANACFN 285
DB 231 LWMVCVLAVFICFVPHVVO-LPWTLAELGY-QTFNHQAINDAHQITLCLLSINCVLDP 288
QY 286 PLIYFAGENFKDLKSLAKRGHPQAKTKC 316
DB 289 FVIYCFLLTKKFKRHLS---EKFYSMRSRKC 316

Search completed: October 8, 2003, 08:30:34
Job time : 102 secs
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RESULT 15

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ID Q8C017 PRELIMINARY; PRT; 341 AA.
AC Q8C017;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Platelet activating factor receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSU=Olfactory brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK032547; BAC27919.1; -.
SQ SEQUENCE 341 AA; 39175 MW; 25F97C6472797386 CRC64;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2003, 08:26:59 ; Search time 21 Seconds
(without alignments)
664.885 Million cell updates/sec

Title: US-09-991-225-2

Perfect score: 1712

Sequence: 1 MEPNGTFNNNSRNCITENF.....KATKCVFVSVWLKRETRV 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PC10S_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1703	99.5	346	4	US-09-585-876-2
2	539	32.7	337	3	US-09-044-404A-2
3	539	32.7	337	4	US-09-586-924-2
4	479	28.0	339	1	US-08-153-848-44
5	479	28.0	339	2	US-08-812-871-3
6	479	28.0	339	3	US-09-299-843A-44
7	479	28.0	339	4	US-09-088-337B-44
8	479	28.0	339	4	US-09-170-496D-32
9	479	28.0	339	5	PC1-US93-11153-44
10	479	28.0	339	5	PC1-US95-07180-2
11	476	27.8	339	4	US-09-170-496D-182
12	461	26.9	362	3	US-08-513-974B-374
13	442	25.8	373	2	US-08-559-524A-4
14	442	25.8	373	3	US-08-749-707-4
15	440	25.7	361	1	US-08-383-750-4
16	440	25.7	361	3	US-08-352-678-4
17	440	25.7	361	4	US-09-536-934-4
18	440	25.7	361	4	US-09-170-496D-78
19	440	25.7	361	5	PC1-US93-09636-4
20	439.5	25.7	348	3	US-08-852-824-17
21	439	25.6	302	2	US-08-467-948A-30
22	439	25.6	302	3	US-08-467-947A-30
23	437	25.5	344	2	US-08-467-948A-8
24	437	25.5	344	3	US-08-467-947A-8
25	434	25.4	361	4	US-09-170-496D-206
26	430	25.1	370	3	US-08-781-250-2
27	419.5	24.5	374	4	US-09-102-710B-3

28	416.5	24.3	373	3	US-08-513-974B-373	Sequence 373, Appl
29	416	24.3	342	3	US-08-988-876-9	Sequence 9, Appl
30	416	24.3	375	1	US-08-442-134A-2	Sequence 2, Appl
31	416	24.3	375	1	US-08-444-581B-2	Sequence 2, Appl
32	416	24.3	375	1	US-08-446-088A-2	Sequence 2, Appl
33	416	24.3	375	1	US-08-559-524A-3	Sequence 3, Appl
34	416	24.3	375	3	US-08-749-707-3	Sequence 3, Appl
35	406.5	23.7	398	1	US-08-097-938-6	Sequence 6, Appl
36	406.5	23.7	398	1	US-08-476-000-6	Sequence 6, Appl
37	406.5	23.7	398	1	US-08-472-840-6	Sequence 6, Appl
38	406.5	23.7	398	2	US-08-476-976-6	Sequence 6, Appl
39	406.5	23.7	398	3	US-08-474-410-6	Sequence 6, Appl
40	405.5	23.7	398	3	US-08-496-673B-6	Sequence 6, Appl
41	405	23.7	355	3	US-09-045-583-53	Sequence 53, Appl
42	405	23.7	355	4	US-09-534-185-53	Sequence 53, Appl
43	401	23.4	347	4	US-08-405-271A-24	Sequence 24, Appl
44	400.5	23.4	398	1	US-08-097-938-4	Sequence 4, Appl
45	400.5	23.4	398	1	US-08-476-000-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-585-876-2
; Sequence 2, Application US/09585876
; Patent No. 6586205
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Slicks-Santiago, Immaculada
; TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 5800-88
; CURRENT APPLICATION NUMBER: US/09/585,876
; CURRENT FILING DATE: 2000-06-01
; EARLIER APPLICATION NUMBER: 60/182,061
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO. 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-585-876-2

Query Match		99.5%;	Score 1703;	DB 4;	Length 346;
Best Local Similarity		99.4%;	Pred. No. 2.1e-124;	Mismatches 1;	Indels 0; Gaps 0;
Matches 328;		Conservative 1;			
QY	1	MEPNGTFNNNSRNCITENFKREPPPIVYLIIFFWGLVGNGLSIYVFTLPYKSTSYNVF	60		
DB	17	MEPNGTFNNNSRNCITENFKREPPPIVYLIIFFWGLVGNGLSIYVFTLPYKSTSYNVF	76		
QY	61	MINLAISDLFIETLEFRADYVLRGWNIGDLACRIMSYSLVNMYSIYFLVLSVVR	120		
DB	77	MINLAISDLFIETLEFRADYVLRGWNIGDLACRIMSYSLVNMYSIYFLVLSVVR	136		
QY	121	FLAWVHFRLIHTYSIRSAWILCGIWIILIMASSIMLLDSGEQNGSVTSCLEMLYKIA	180		
DB	137	FLAWVHFRLIHTYSIRSAWILCGIWIILIMASSIMLLDSGEQNGSVTSCLEMLYKIA	196		
QY	181	KIQPMNIALVWGCILPFTTSLICVILLIRVLLKVEVPESGLRVSHRKALTIITLIIF	240		
DB	197	KIQPMNIALVWGCILPFTTSLICVILLIRVLLKVEVPESGLRVSHRKALTIITLIIF	256		
QY	241	FICFLPHTLRTVHLTTWKVGLCKDRHLKALVTTLAANAACFNPLLYIFAGNFKDLR	300		
DB	257	FICFLPHTLRTVHLTTWKVGLCKDRHLKALVTTLAANAACFNPLLYIFAGNFKDLR	316		
QY	301	KSALRKGHPQAKTKCVFVSVWLKRETRV	330		
DB	317	KSALRKGHPQAKTKCVFVSVWLKRETRV	346		


```

; TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-153-848-44

Query Match 28.0%; Score 479; DB 1; Length 339;
Best Local Similarity 34.8%; Pred. No. 6.8e-30;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

Qy 7 FSNNSRNCIEN-FKREFPIVILIIFFWGLNGLSIYVFLQPKKSTSVNFMNLA 65
Db 15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLTALWLFIRHKGSTPANVFMHLA 74
Qy 66 ISDLFTSTLPFRADYILGSGNWIFGDLACRIMSISLYVNMYSIYVFLVLSVVRFLAV 125
Db 75 VADLSCVLVLPTRLVYHFGSNHWPFGEIACRLGFLFLNMYASIFLTCISADRFIAIV 134
Qy 126 HPFRLHVTTSIRSAWILCGIITWLI-MASSTMLDSDSGEONGSVTSCLELNLYKIAKLOT 184
Db 135 HPVKSILRRPLAHLACAFLLVWVAVAMAPLLVSPQVTQNTNHTVVCLO--LYR-EKASH 191
Qy 185 MNYIALVVGCLLPFFLSICYLLIIRVLLKVEPEGLRVSHR---KALTWIIITLIIF 241
Db 192 HALVSLAVAFEPFITTVCYLLIIRSL-----ROGLRVEKRLKTKAVRMIAIVLAI 245
Qy 242 LCFPLPYHLRTVHLTKV--GLCKDRHLKALV--ITLALAAANACFNPLIYYPAGNFK 297
Db 246 VCFVPYHVNRSYIVLHYRSHGASCATQIRILALANRITSCLTSLNGALDPIWFFVAKFR 305
Qy 298 DRKLSAL----RKGHPOKAKTK 315
Db 306 HALCNLLCGKRLKGPSPPEGK 327

RESULT 5
US-08-812-871-3
; Sequence 3, Application US/08812871
; Patent No. 5955303
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice

```

```

; APPLICANT: Guegler, Karl
; APPLICANT: Muzong Cheng
; TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,871
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0237 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 992700
; US-08-812-871-3

Query Match 28.0%; Score 479; DB 2; Length 339;
Best Local Similarity 34.8%; Pred. No. 6.8e-30;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

Qy 7 FSNNSRNCIEN-FKREFPIVILIIFFWGLNGLSIYVFLQPKKSTSVNFMNLA 65
Db 15 FSLATAEQCGQETPLENMLFASFYLLDFILALVGNLTALWLFIRHKGSTPANVFMHLA 74
Qy 66 ISDLFTSTLPFRADYILGSGNWIFGDLACRIMSISLYVNMYSIYVFLVLSVVRFLAV 125
Db 75 VADLSCVLVLPTRLVYHFGSNHWPFGEIACRLGFLFLNMYASIFLTCISADRFIAIV 134
Qy 126 HPFRLHVTTSIRSAWILCGIITWLI-MASSTMLDSDSGEONGSVTSCLELNLYKIAKLOT 184
Db 135 HPVKSILRRPLAHLACAFLLVWVAVAMAPLLVSPQVTQNTNHTVVCLO--LYR-EKASH 191
Qy 185 MNYIALVVGCLLPFFLSICYLLIIRVLLKVEPEGLRVSHR---KALTWIIITLIIF 241
Db 192 HALVSLAVAFEPFITTVCYLLIIRSL-----ROGLRVEKRLKTKAVRMIAIVLAI 245
Qy 242 LCFPLPYHLRTVHLTKV--GLCKDRHLKALV--ITLALAAANACFNPLIYYPAGNFK 297
Db 246 VCFVPYHVNRSYIVLHYRSHGASCATQIRILALANRITSCLTSLNGALDPIWFFVAKFR 305
Qy 298 DRKLSAL----RKGHPOKAKTK 315
Db 306 HALCNLLCGKRLKGPSPPEGK 327

RESULT 6
US-09-299-843A-44

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Query Match	28.0%	Score	479;	DB	3;	Length	339;		
Best Local Similarity	34.8%	Pred.	No. 6.8e-30;						
Matches	112;	Conservative	62;	Mismatches	126;	Indels	22;	Gaps	9;
QY	7	FSNNNSRNCIEN-EKREFFPIVLIIFFGVLGRLGLSIYVFLQPKYKTSVNVFNLIA	65						
Db	15	PSLATAQCCQGTPEENMLPASFYLDLIALVGNLTALWLFIKHSKGPANVFLMLHA	74						
QY	66	ISDLPISTILPRADYILRGSNWTFGLDAGRMSYSLAVNYSYISYFLTVLSVFLVAV	125						
Db	75	VADLSCVLIPRLVYHSGHNHFFGEIACRLTGLFVFLNMYASIFLPTCISADRELAIV	134						
QY	126	HPFRLHVTISRSANTLGGIIWILI-NASSIMLLDGSSEQNGSVTSCLENLNIIKYAKLOT	184						
Db	135	HPVKSLLRRPLAYHACAFVWVAVAMAPLIVSPQTVQTNHTWVCIQ-LYR-EKASH	191						
QY	185	KNYALVGVGLPFPTLSTCYLLIIRVLLKAVEPESGLRVSHR--FALFTIILITLFF	241						
Db	192	HALVSVAEATFPFTITVTCZLLIIRSL-----ROGLRVKRLKTVARMLIAVLIAFL	245						
QY	242	LCFUFYHTLTVHLTATWKV--GLCKDRLHRLV-ITTLAALAAACFNPLIYFAGENFK	297						
Db	246	VCFFPYHNVNSVYLYHSHGASCATORILALANRTSCLTSLNGALDPIINPFVAKFR	305						

[illegible]


```
/ ADDRESSEE: STEWART & OLSTEIN
/ STREET: 6 BECKER FARM ROAD
/ CITY: ROSELAND
/ STATE: NJ
/ COUNTRY: US
/ ZIP: 07068
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/07180
/ FILING DATE: 06-JUNE-1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MULLINS, J.G.
/ REGISTRATION NUMBER: 30,073
/ REFERENCE/DOCKET NUMBER: 325800-366
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-994-1700
/ TELEFAX: 201-994-1744
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 339 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US95-07180-2

Query Match      28.0%; Score 479; DB 5; Length 339;
Best Local Similarity 34.8%; Pred. No. 6.8e-30;
Matches 112; Conservative 62; Mismatches 126; Indels 22; Gaps 9;

QY  7 FSNNSNCTIEN-FKREFFPIVILIIFPWGVLGNLSIYVLPQPKKSTSVNFMNLNLA 65
DB  15 FSLATAQCQGTPLENMLFASFYLLDFILALVGNLALMLFIRDHKGSTPANVFIMHLA 74
QY  66 ISDLFTSTLPPRADYILGRSNWIFGDLACRIMSYSLYVMYSSIVFTLVSVRFLAMV 125
DB  75 VADLSCLVLPFLVLYHFSNGHWPGEIACRLTGFLYLNMYASIVFTLCISADRELAIV 134
QY  126 HPFRLHVTSIRSANILCGIITWLI-MASSIMLDGSGEQSVTSCLELNLYKIAKLT 184
DB  135 HPVKSRLRPIYLAHLACAFLLWVAVAMAPLLVSPQVTQNTHTVVCLO--LYR-EKASH 191
QY  185 MNYIALVVGCLLPPFTLSTCYLLIIRVLLKVEVPESGLRVSHR---KALTITIIITLIIF 241
DB  192 HALVSLAVATFTFTVTCYLLIIRSL-----RGLRVERKELTKAKRMIAIVLAIFL 245
QY  242 LCLFPHYTLRTVHLTWKY--GLCKDRHLKALV--ITLALAAANACFNPLLYFAGENFK 297
DB  246 VCFVPHVNRSVVLYHRSHGASCATQRIALANRITSCLTSLNGALDPTIMFFVAEKFR 305
QY  298 DELKSAL----RKGHPOKATK 315
DB  306 HALCNLCGKRLKGPPSPFEK 327

RESULT 11
US-09-170-496D-182
; Sequence 182, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170/496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
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/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 182
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-170-496D-182

Query Match      27.8%; Score 476; DB 4; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 61; Mismatches 127; Indels 22; Gaps 9;

QY  7 FSNNSNCTIEN-FKREFFPIVILIIFPWGVLGNLSIYVLPQPKKSTSVNFMNLNLA 65
DB  15 FSLATAQCQGTPLENMLFASFYLLDFILALVGNLALMLFIRDHKGSTPANVFIMHLA 74
QY  66 ISDLFTSTLPPRADYILGRSNWIFGDLACRIMSYSLYVMYSSIVFTLVSVRFLAMV 125
DB  75 VADLSCLVLPFLVLYHFSNGHWPGEIACRLTGFLYLNMYASIVFTLCISADRELAIV 134
QY  126 HPFRLHVTSIRSANILCGIITWLI-MASSIMLDGSGEQSVTSCLELNLYKIAKLT 184
DB  135 HPVKSRLRPIYLAHLACAFLLWVAVAMAPLLVSPQVTQNTHTVVCLO--LYR-EKASH 191
QY  185 MNYIALVVGCLLPPFTLSTCYLLIIRVLLKVEVPESGLRVSHR---KALTITIIITLIIF 241
DB  192 HALVSLAVATFTFTVTCYLLIIRSL-----RGLRVERKELTKAKRMIAIVLAIFL 245
QY  242 LCLFPHYTLRTVHLTWKY--GLCKDRHLKALV--ITLALAAANACFNPLLYFAGENFK 297
DB  246 VCFVPHVNRSVVLYHRSHGASCATQRIALANRITSCLTSLNGALDPTIMFFVAEKFR 305
QY  298 DRKSAL----RKGHPOKATK 315
DB  306 HALCNLCGKRLKGPPSPFEK 327

RESULT 12
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 374:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-513-974B-374

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Query Match 26.9%; Score 461; DB 3; Length 362;
Best Local Similarity 30.7%; Pred. No. 1.8e-28;
Matches 98; Conservative 81; Mismatches 114; Indels 26; Gaps 7;

QY 5 GTFSNNRSNCTI--ENFKREFFPIVYLIIFFWGVLGNSLSYIVLPQYKSTSVNFM 62
Db 21 GWAAGNATTKCSITKTKGFQFYLLPTVILVFITGLGNSVAILWVFVHMRPWSGISYMF 80

QY 63 NLAISDLIFSTLFFRADYILRGSNWIFGDLACRIMSISLYVNMYSIVFTLVLSVVRFL 122
Db 81 NLAALDFLYLTLPALIFYFNKTDWIFGDMCKLQRFIFHVNKXGSLFTLCISVHRYT 140

QY 123 ANVHFFRLHVTISRANILCGIILWIMASSIMLL---DSGSEONGSVTSCLE----- 173
Db 141 GVWPLKSLGRLKKNVAVSSLVWALVAVIAPILFYSIGVGRNKKIT-CYDTTAD 199

QY 174 LNLKYIAKLTQMNIALVWGCLLPFTLSICVLLIIRVLKVEPESGLRYSHERKALT 233
Db 200 LSEFVVSMTTTFVNCI-----TFVILGCGILVVALIYKLDNSPLR---RKSYLV 251

QY 234 IITLHIFLFCPLPHYLRVHL-----TTWKVGLCKDRHLKALVITLALAAACFNPL 287
Db 252 IIVLTVPVAVSLPHVVKTLNLRARLDFTQPMCAFNDKVIATYQVTRGLASLNSCDPI 311

QY 288 LYFAGENFKDRKLSLRK 306
Db 312 LYFLAGDTFRRLSRATRK 330

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RESULT 13
US-08-559-524A-4

```

```

; Sequence 4, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,524A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044461-5010-00-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-559-524A-4

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Query Match 25.8%; Score 442; DB 2; Length 373;
Best Local Similarity 31.0%; Pred. No. 5.4e-27;
Matches 95; Conservative 78; Mismatches 109; Indels 24; Gaps 7;

QY 16 TIENKREPPYVLIIRPFWGLNGLSIVYFLOPKYKSTSVNFMALNALSLEFISTL 75
Db 45 TKTGFQYYPVAYIIVFIFGLGNSVAILWVFVHMRPWSGISVTFMRLADEFLVITL 104

QY 76 PFRADYILRGSNWIFGDLACRIMSISLYVNMYSIVFTLVLSVVRFLAMVHPPFLHVT 135
Db 105 PALIFYFNKTDWIFGDMCKLQRFIFHVNKXGSLFTLCISAHRYSGVWYPLKSLGR 164

QY 136 IRSAWILCGIITWILIMASSIMLL---DSGSEONGSVTSCLE-----LNLKYIAKLTQMN 186
Db 165 KKNVAVISLVWLVVGVISPLFYSIGVGRNKKIT-CYDTTDSYLRYSFYSMCT-- 221

QY 187 YIALVWGCLLPFTLSICVLLIIRVLKVEPESGLRYSHERKALTIIITLIIFFLCFLP 246
Db 222 --TVAMEFC-VPIVILGCVGLIVRALIYKLDNSPLR---RKSIYLVITLVFANSYIP 275

QY 247 YHTRTVHL-----TTWKVGLCKDRHLKALVITLALAAACFNPLIYFAGENFKDR 300
Db 276 FHVVKTLNLRARLDFTQPMCAFNDKVIATYQVTRGLASLNSCDVPIYFLAGDTFRRL 335

QY 301 KSLARK 306
Db 336 SRATRK 341

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RESULT 14
US-08-749-707-4
; Sequence 4, Application US/08749707
; Patent No. 6063582
; GENERAL INFORMATION:

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2003, 08:27:32 ; Search time 30 Seconds
(without alignments)
1772.413 Million cell updates/sec

Title: US-09-991-225-2

Perfect score: 1712

Sequence: 1 MEPNGTFSNNRNCTIENF.....KATKCVFVSVWLKRETRV 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1712	100.0	330	9	US-09-826-791-2
2	1712	100.0	330	12	US-09-991-225-2
3	1712	100.0	341	12	US-09-991-225-55
4	1712	100.0	346	9	US-09-826-791-6
5	1712	100.0	346	10	US-09-866-230-7
6	1712	100.0	346	10	US-09-866-230-9
7	1712	100.0	346	10	US-09-828-478-2
8	1712	100.0	346	11	US-09-779-679-2
9	1712	100.0	346	11	US-09-779-679-26
10	1712	100.0	346	12	US-09-991-225-30
11	1712	100.0	346	12	US-10-349-021-2
12	1712	100.0	346	12	US-10-321-807-14
13	1712	100.0	346	15	US-10-225-567A-589
14	1706	99.6	346	12	US-10-321-807-88
15	564	32.9	337	15	US-10-225-567A-304

16	559	32.7	337	10	US-09-866-230-8	Sequence 8, Appli
17	559	32.7	337	10	US-09-828-478-5	Sequence 5, Appli
18	559	32.7	337	11	US-09-779-679-27	Sequence 27, Appl
19	559	32.7	337	12	US-09-991-225-6	Sequence 6, Appli
20	559	32.7	337	12	US-10-349-021-5	Sequence 5, Appli
21	559	32.7	337	15	US-10-225-567A-547	Sequence 547, Appl
22	557	32.5	337	15	US-10-167-192-3	Sequence 3, Appli
23	487.5	28.5	337	9	US-09-943-798-4	Sequence 4, Appli
24	487.5	28.5	337	11	US-09-885-453-1	Sequence 1, Appli
25	487.5	28.5	337	12	US-10-017-161-526	Sequence 526, App
26	487.5	28.5	337	12	US-10-278-141-2	Sequence 2, Appli
27	487.5	28.5	337	12	US-10-010-568-2	Sequence 2, Appli
28	487.5	28.5	337	12	US-10-321-807-28	Sequence 28, Appl
29	487.5	28.5	337	15	US-10-023-775B-2	Sequence 2, Appli
30	487.5	28.5	337	15	US-10-270-144-2	Sequence 2, Appli
31	487.5	28.5	337	15	US-10-188-405-8	Sequence 8, Appli
32	487.5	28.5	337	15	US-10-079-384-14	Sequence 14, Appl
33	485.5	28.4	337	15	US-10-225-567A-647	Sequence 647, App
34	479	28.0	339	9	US-09-848-889-12	Sequence 12, Appl
35	479	28.0	339	9	US-09-788-133-2	Sequence 2, Appli
36	479	28.0	339	10	US-09-828-478-4	Sequence 4, Appli
37	479	28.0	339	12	US-09-991-225-8	Sequence 8, Appli
38	479	28.0	339	12	US-10-349-021-4	Sequence 4, Appli
39	479	28.0	339	12	US-10-100-982-12	Sequence 12, Appl
40	479	28.0	339	12	US-10-268-332-14	Sequence 14, Appl
41	479	28.0	339	12	US-09-964-821B-14	Sequence 14, Appl
42	479	28.0	339	15	US-10-251-385-32	Sequence 32, Appl
43	479	28.0	367	10	US-09-828-478-6	Sequence 6, Appli
44	479	28.0	367	12	US-10-349-021-6	Sequence 6, Appli
45	479	28.0	367	15	US-10-225-567A-304	Sequence 304, App

ALIGNMENTS

RESULT 1
US-09-826-791-2
; Sequence 2, Application US/09826791
; Patent No. US20010039037A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc
; TITLE OF INVENTION: No. US20010039037A1el Polypeptide
; FILE REFERENCE: PC10914ADAM
; CURRENT APPLICATION NUMBER: US/09/826,791
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 0008504.3
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/198,367
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO. 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-791-2

Query Match 100.0%; Score 1712; DB 9; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.1e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPNGTFSNNRNCTIENFKEFFPIYLIIFWGLNGLSIYVFLQPKKTSVNVF 60

Db 1 MEPNGTFSNNRNCTIENFKEFFPIYLIIFWGLNGLSIYVFLQPKKTSVNVF 60

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Db 61 MLNLAISDLFIETLPRADYILRGSNWFGLDLCRIMSYLYVMYSIYFLVLSVR 120

Qy 121 FLAVVHFRLLHVTSTRSAILCGIITWILIMASSIMLLDSGEQNGSVTSCLELNKIA 180

Db 121 FLAVVHFRLLHVTSTRSAILCGIITWILIMASSIMLLDSGEQNGSVTSCLELNKIA 180

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QY 181 KLOTNMYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
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Db 181 KLOTNMYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
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QY 241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYFAGENFKDRL 300
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Db 241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYFAGENFKDRL 300
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QY 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
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Db 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
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RESULT 2
US-09-991-225-2
; Sequence 2, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY11, EXPRESSED IN
; FILE REFERENCE: D0075.NP
; CURRENT APPLICATION NUMBER: US/09/991.225
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-991-225-2

Query Match 100.0%; Score 1712; DB 12; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.1e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 FLAMVHFFRLLHVTISRANILGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
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QY 241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYFAGENFKDRL 300
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QY 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
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RESULT 3
US-09-991-225-55
; Sequence 55, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
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; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY11, EXPRESSE
; FILE REFERENCE: D0075.NP
; CURRENT APPLICATION NUMBER: US/09/991.225
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-225-55

Query Match 100.0%; Score 1712; DB 12; Length 341;
Best Local Similarity 100.0%; Pred. No. 1.1e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 MLNLAISDLLFISTLPFRADYILRGSNWIFGDLACRIMSYSLYVNMKSSYVFTVLSVVR 120
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Db 72 MLNLAISDLLFISTLPFRADYILRGSNWIFGDLACRIMSYSLYVNMKSSYVFTVLSVVR 131
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QY 121 FLAMVHFFRLLHVTISRANILGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
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Db 132 FLAMVHFFRLLHVTISRANILGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 191
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QY 181 KLOTNMYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
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Db 192 KLOTNMYIALVVGCLLPFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 251
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QY 241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYFAGENFKDRL 300
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Db 252 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYFAGENFKDRL 311
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QY 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
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Db 312 KSALRGHPQAKTKCVFPVSVWLKRETRV 341
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RESULT 4
US-09-826-791-6
; Sequence 6, Application US/09826791
; Patent No. US20010039037A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc
; TITLE OF INVENTION: No. US20010039037A1e1 Polypeptide
; FILE REFERENCE: PC10914ADAM
; CURRENT APPLICATION NUMBER: US/09/826,791
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 0008504.3
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/198,367
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-791-6

Query Match 100.0%; Score 1712; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MEPNGTFSNNNSRNCNTIENFKREFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNVF 60
Db 17 MEPNGTFSNNNSRNCNTIENFKREFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNVF 76
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Db 77 MNLAISDLLFIPTLPFRADYLRGNSWIFGDLACRIMSYSLYVNMYSYIFLTVLSVVR 136
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Db 137 FLAMVHPFRLHVTISRSAWILCGIWIILIMASSIMLDGSGONGSVTSCLELNLYKIA 196
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Db 317 KSALRGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 5

US-09-866-230-7
; Sequence 7, Application US/09866230
; Patent No. US20020150901A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Andrew, et al.
; TITLE OF INVENTION: No. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Making
; FILE REFERENCE: REG 771A
; CURRENT APPLICATION NUMBER: US/09/866,230
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,725
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-230-7

Query Match 100.0%; Score 1712; DB 10; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPNGTFSNNNSRNCNTIENFKREFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNVF 60
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QY 61 MNLAISDLLFIPTLPFRADYLRGNSWIFGDLACRIMSYSLYVNMYSYIFLTVLSVVR 120
Db 77 MNLAISDLLFIPTLPFRADYLRGNSWIFGDLACRIMSYSLYVNMYSYIFLTVLSVVR 136
QY 121 FLAMVHPFRLHVTISRSAWILCGIWIILIMASSIMLDGSGONGSVTSCLELNLYKIA 180
Db 137 FLAMVHPFRLHVTISRSAWILCGIWIILIMASSIMLDGSGONGSVTSCLELNLYKIA 196
QY 181 KLOTMYIALVVGCLLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
Db 197 KLOTMYIALVVGCLLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256
QY 241 FLCFLPYHTLRVTLTWTWKVGLCKDRHLKALVTITLALAAANACFPNLLYFAGENFKDRL 300
Db 257 FLCFLPYHTLRVTLTWTWKVGLCKDRHLKALVTITLALAAANACFPNLLYFAGENFKDRL 316
QY 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
Db 317 KSALRGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 6

US-09-866-230-9
; Sequence 9, Application US/09866230
; Patent No. US20020150901A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Andrew, et al.
; TITLE OF INVENTION: No. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Making
; FILE REFERENCE: REG 771A
; CURRENT APPLICATION NUMBER: US/09/866,230
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,725
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-230-9

Query Match 100.0%; Score 1712; DB 10; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPNGTFSNNNSRNCNTIENFKREFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNVF 60
Db 17 MEPNGTFSNNNSRNCNTIENFKREFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNVF 76
QY 61 MNLAISDLLFIPTLPFRADYLRGNSWIFGDLACRIMSYSLYVNMYSYIFLTVLSVVR 120
Db 77 MNLAISDLLFIPTLPFRADYLRGNSWIFGDLACRIMSYSLYVNMYSYIFLTVLSVVR 136
QY 121 FLAMVHPFRLHVTISRSAWILCGIWIILIMASSIMLDGSGONGSVTSCLELNLYKIA 180
Db 137 FLAMVHPFRLHVTISRSAWILCGIWIILIMASSIMLDGSGONGSVTSCLELNLYKIA 196
QY 181 KLOTMYIALVVGCLLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
Db 197 KLOTMYIALVVGCLLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256
QY 241 FLCFLPYHTLRVTLTWTWKVGLCKDRHLKALVTITLALAAANACFPNLLYFAGENFKDRL 300
Db 257 FLCFLPYHTLRVTLTWTWKVGLCKDRHLKALVTITLALAAANACFPNLLYFAGENFKDRL 316
QY 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
Db 317 KSALRGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 7

US-09-828-478-2
; Sequence 2, Application US/09828478
; Patent No. US20020155528A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; FILE REFERENCE: 04974, 00458
; CURRENT APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-478-2

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; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-679--2

Query Match      100.0%; Score 1712; DB 11; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB   17  MEPNGTFSNNNSRNCIENFKREFFPIVYLITFFMGVLGNGLSIYYFLQPYPKKSISYNVF 76
    |||

QY   61  MNLAISDLFIETLPRADYYLRGSNWIPGDLCACRMISLSLYVMYSIFLVLSVVR 120
    |||
DB   77  MNLAISDLFIETLPRADYYLRGSNWIPGDLCACRMISLSLYVMYSIFLVLSVVR 136
    |||

QY   121 FLAMVHPFLLHVTIRSRAWILCGIIWLIMASSLMILDGSGPONGSVTSCLLENLYKIA 180
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DB   137 FLAMVHPFLLHVTIRSRAWILCGIIWLIMASSLMILDGSGPONGSVTSCLLENLYKIA 196
    |||

QY   181 KIQCTNYIALWGCLLPFFTISICVLLIRVILKVEVPESGLRVSHRKALTITITLIIF 240
    |||
DB   197 KIQCTNYIALWGCLLPFFTISICVLLIRVILKVEVPESGLRVSHRKALTITITLIIF 256
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QY   241 FLCFTPYTLTTHVLTTWKVGLCKDRLUHKALVITITALAANACPENFLIYPAGNFKNDR 300
    |||
DB   257 FLCFTPYTLTTHVLTTWKVGLCKDRLUHKALVITITALAANACPENPLLIYPAGNFKNDR 316
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QY   301 KSALKRGHPQAKTKCVFPVSFWLKETRV 330
DB   317 KSALKRGHPQAKTKCVFPVSFWLKETRV 346
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; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: USSN 60/181157
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 26
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-679-26

Query Match      100.0%; Score 1712; DB 11; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPNGTFSNNRNCTIENFKREFPIVYLLIIFWGLNGLSIYVFLQPKKSTSYNVF 60
DB 17 MEPNGTFSNNRNCTIENFKREFPIVYLLIIFWGLNGLSIYVFLQPKKSTSYNVF 76

QY 61 MNLAISDLLFIETLPFRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLVLSVR 120
DB 77 MNLAISDLLFIETLPFRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLVLSVR 136

QY 121 FLAMVHPRLLHVTISRANILCGIILWILIMASSIMLLDSGSEQNGSVTSCLEINLYKIA 180
DB 137 FLAMVHPRLLHVTISRANILCGIILWILIMASSIMLLDSGSEQNGSVTSCLEINLYKIA 196

QY 181 KLOTMYNIALVVGCLLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
DB 197 KLOTMYNIALVVGCLLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

QY 241 FLCPLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACFNPLLYYPAGENFKDRL 300
DB 257 FLCPLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACFNPLLYYPAGENFKDRL 316

QY 301 KSALRKGHPQAKTKCVFPVSVWLKRETRV 330
DB 317 KSALRKGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 10
US-09-991-225-30
; Sequence 30, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPFRM11, EXPRESSED HI
; FILE REFERENCE: D0075.NP
; CURRENT APPLICATION NUMBER: US/09/991,225
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 30
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-225-30

Query Match      100.0%; Score 1712; DB 12; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 17 MEPNGTFSNNRNCTIENFKREFPIVYLLIIFWGLNGLSIYVFLQPKKSTSYNVF 76

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QY 61 MNLAISDLLFIETLPFRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLVLSVR 120
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QY 121 FLAMVHPRLLHVTISRANILCGIILWILIMASSIMLLDSGSEQNGSVTSCLEINLYKIA 180
DB 137 FLAMVHPRLLHVTISRANILCGIILWILIMASSIMLLDSGSEQNGSVTSCLEINLYKIA 196

QY 181 KLOTMYNIALVVGCLLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
DB 197 KLOTMYNIALVVGCLLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

QY 241 FLCPLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACFNPLLYYPAGENFKDRL 300
DB 257 FLCPLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACFNPLLYYPAGENFKDRL 316

QY 301 KSALRKGHPQAKTKCVFPVSVWLKRETRV 330
DB 317 KSALRKGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 11
US-10-349-021-2
; Sequence 2, Application US/10349021
; Publication No. US20030157541A1
; GENERAL INFORMATION:
; APPLICANT: xiao, fonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/10/349,021
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-349-021-2

Query Match      100.0%; Score 1712; DB 12; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPNGTFSNNRNCTIENFKREFPIVYLLIIFWGLNGLSIYVFLQPKKSTSYNVF 60
DB 17 MEPNGTFSNNRNCTIENFKREFPIVYLLIIFWGLNGLSIYVFLQPKKSTSYNVF 76

QY 61 MNLAISDLLFIETLPFRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLVLSVR 120
DB 77 MNLAISDLLFIETLPFRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLVLSVR 136

QY 121 FLAMVHPRLLHVTISRANILCGIILWILIMASSIMLLDSGSEQNGSVTSCLEINLYKIA 180
DB 137 FLAMVHPRLLHVTISRANILCGIILWILIMASSIMLLDSGSEQNGSVTSCLEINLYKIA 196

QY 181 KLOTMYNIALVVGCLLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 240
DB 197 KLOTMYNIALVVGCLLPFTLSICYLIIIRVLLKVEVPESGLRVSHRKALTTIITLIIF 256

QY 241 FLCPLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACFNPLLYYPAGENFKDRL 300
DB 257 FLCPLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACFNPLLYYPAGENFKDRL 316

QY 301 KSALRKGHPQAKTKCVFPVSVWLKRETRV 330
DB 317 KSALRKGHPQAKTKCVFPVSVWLKRETRV 346

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RESULT 12
US-10-321-807-14
; Sequence 14, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Rupong
; APPLICANT: Bang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 14
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-807-14

Query Match      100.0%; Score 1712; DB 12; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MEPNGTFSNNRNCTIENKREFFPIVYLIIFFWGLNGLSIYVFLQPKKSTSVNF 60
      |||||||
Db      17  MEPNGTFSNNRNCTIENKREFFPIVYLIIFFWGLNGLSIYVFLQPKKSTSVNF 76
      |||||||

QY      61  MLNLAISDLFI STLPRADYLRGWNIFGDLACRIMSYSLYVNMYSIYFVLVSVVR 120
      |||||||
Db      77  MLNLAISDLFI STLPRADYLRGWNIFGDLACRIMSYSLYVNMYSIYFVLVSVVR 136
      |||||||

QY      121  FLAMVHPEFLHVTISRGAWILCGIWIILMASSIMLDGSEONGSVTSCLELNLYKTA 180
      |||||||
Db      137  FLAMVHPEFLHVTISRGAWILCGIWIILMASSIMLDGSEONGSVTSCLELNLYKTA 196
      |||||||

QY      181  KLQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIF 240
      |||||||
Db      197  KLQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIF 256
      |||||||

QY      241  FLCFLPYHTLRTVHLTKVGLCKDRHLKALVTTLAANAACFNPLLYTFAGENFKDRL 300
      |||||||
Db      257  FLCFLPYHTLRTVHLTKVGLCKDRHLKALVTTLAANAACFNPLLYTFAGENFKDRL 316
      |||||||

QY      301  KSALRKGHPQAKTKCVFPVSVWLKRETRV 330
      |||||||
Db      317  KSALRKGHPQAKTKCVFPVSVWLKRETRV 346
      |||||||

US-10-321-807-14
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RESULT 13
US-10-225-567A-589
; Sequence 589, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Roush, Christine L.
; APPLICANT: Burmer, Glenn C.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECP
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 589
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-589

Query Match      100.0%; Score 1712; DB 15; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.2e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MEPNGTFSNNRNCTIENKREFFPIVYLIIFFWGLNGLSIYVFLQPKKSTSVNF 60
      |||||||
Db      17  MEPNGTFSNNRNCTIENKREFFPIVYLIIFFWGLNGLSIYVFLQPKKSTSVNF 76
      |||||||

QY      61  MLNLAISDLFI STLPRADYLRGWNIFGDLACRIMSYSLYVNMYSIYFVLVSVVR 120
      |||||||
Db      77  MLNLAISDLFI STLPRADYLRGWNIFGDLACRIMSYSLYVNMYSIYFVLVSVVR 136
      |||||||

QY      121  FLAMVHPEFLHVTISRGAWILCGIWIILMASSIMLDGSEONGSVTSCLELNLYKTA 180
      |||||||
Db      137  FLAMVHPEFLHVTISRGAWILCGIWIILMASSIMLDGSEONGSVTSCLELNLYKTA 196
      |||||||

QY      181  KLQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIF 240
      |||||||
Db      197  KLQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIF 256
      |||||||

QY      241  FLCFLPYHTLRTVHLTKVGLCKDRHLKALVTTLAANAACFNPLLYTFAGENFKDRL 300
      |||||||
Db      257  FLCFLPYHTLRTVHLTKVGLCKDRHLKALVTTLAANAACFNPLLYTFAGENFKDRL 316
      |||||||

QY      301  KSALRKGHPQAKTKCVFPVSVWLKRETRV 330
      |||||||
Db      317  KSALRKGHPQAKTKCVFPVSVWLKRETRV 346
      |||||||

US-10-321-807-88
; Sequence 88, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Rupong
; APPLICANT: Bang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Humal
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
```



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XX PA (HARL/) HARLAND L.
XX PI Harland L;
XX DR WPI: 2002-040722/05.
XX DR N-PSDB; AAH77276.
XX
XX New PFI-017 protein and polynucleotide encoding the protein, useful for
XX diagnosing or treating metabolic diseases, urogenital disease,
XX immunological disorders, infectious diseases, neoplastic or
XX myeloproliferative diseases -
XX
XX Claim 7; Fig 6B; 39pp; English.
XX
XX The sequence represents a novel G-protein coupled receptor (GPCR),
XX PFI-017 of the invention. The PFI-017 has cytostatic, antiallergic,
XX osteopathic, cardiovascular, and immunosuppressive activity. The
XX polynucleotides may have a use in gene therapy. The polynucleotide is
XX useful for treating allergic disorders, an inflammatory disorder, an
XX immunological disorder, a pulmonary disorder, an infectious disease, a
XX neoplastic or myeloproliferative disease, or a heart disease. The
XX allergic disorder is an allergic rhinitis or asthma, the pulmonary
XX disease is COPD, and the inflammatory disorder is inflammatory bowel
XX disease. PFI-017 polynucleotide sequences may be used for the diagnosis
XX of diseases resulting from expression of PFI-017, and to detect and
XX quantify gene expression in conditions, disorders or diseases in which
XX PFI-017 activity may be implicated. The polypeptides are used to produce
XX anti-PFI-017 antibodies to be used diagnostically to detect and quantify
XX PFI-017 levels in disease states. The antibodies, compounds and
XX compositions which can modulate the peptide can be used in treating
XX obesity, diabetes and metabolic disease, neurological disease, urogenital
XX disease, inflammation, cancer, osteoporosis, cardiovascular disease,
XX gastrointestinal disease, infections, allergy and respiratory disease,
XX sensory organ disorders, sleep disorders, hair loss, immunological
XX disorders, pulmonary diseases, infectious diseases, neoplastic and
XX myeloproliferative diseases, vasculitic granulomatous diseases, and heart
XX diseases. These may also be used in dermatology, and psychotherapeutics.
XX
XX Sequence 330 AA:
XX
XX Query Match 100.0%; Score 1712; DB 23; Length 330;
XX Best Local Similarity 100.0%; Pred. No. 5.4e-177;
XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MEPNGTFSNNRNCTIENKREFFPIVYLIIFFWGLNGLSIYVFLQPKKTSVNVF 60
XX |||||
XX Db 1 MEPNGTFSNNRNCTIENKREFFPIVYLIIFFWGLNGLSIYVFLQPKKTSVNVF 60
XX
XX QY 61 MLMLAISDLLFISLTPRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLTVLSVVR 120
XX |||||
XX Db 61 MLMLAISDLLFISLTPRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLTVLSVVR 120
XX
XX QY 121 FLAMVHFFLLHVTISRSANILCGIITWILIMASSIMLMDSGSENGSVTSCLLENLYKIA 180
XX |||||
XX Db 121 FLAMVHFFLLHVTISRSANILCGIITWILIMASSIMLMDSGSENGSVTSCLLENLYKIA 180
XX
XX QY 181 KLQTMNYIALVVGCLLPFFLSICYLLIIRVILVKYVEPSGLRVSHRKALTIITLIIIF 240
XX |||||
XX Db 181 KLQTMNYIALVVGCLLPFFLSICYLLIIRVILVKYVEPSGLRVSHRKALTIITLIIIF 240
XX
XX QY 241 FLCFLYHTRVHLVHTWKVGLCKDRHLKALVITILAAANACFNPLIIYFAGEFKDRL 300
XX |||||
XX Db 241 FLCFLYHTRVHLVHTWKVGLCKDRHLKALVITILAAANACFNPLIIYFAGEFKDRL 300
XX
XX QY 301 KSALRGHPQKAKTCKVPPSVWLKRETRV 330
XX |||||
XX Db 301 KSALRGHPQKAKTCKVPPSVWLKRETRV 330
XX
XX RESULT 2
XX ABU11900
XX ID ABU11900 standard; Protein; 330 AA.

```

```

XX AC ABU11900;
XX XX
XX DT 13-FEB-2003 (first entry)
XX XX
XX DE Human G-protein coupled receptor HGPRBMY11.
XX XX
XX KW Human; receptor; HGPRBMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
XX KW G-protein coupled receptor; cardiovascular disease; arrhythmia;
XX KW myocardial infarction; congestive heart failure; cardiomyopathy;
XX KW atherosclerosis; arteriosclerosis; embolism; angina; thrombosis;
XX KW hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis;
XX KW obesity; human immunodeficiency virus infection; HIV; schizophrenia;
XX KW sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.
XX KW Homo sapiens.
XX OS
XX XX
XX PN WC2002086123-A2.
XX XX
XX PD 31-OCT-2002.
XX XX
XX XX 16-NOV-2001; 2001WO-US44019.
XX XX
XX XX 17-NOV-2000; 2000US-249613P.
XX XX
XX PR 21-DEC-2000; 2000US-257611P.
XX PR
XX PR 16-JUL-2001; 2001US-305818P.
XX XX
XX XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX FA
XX XX
XX PI Feder J, Nelson TC, Ramanathan C, Cacace AM, Barber LE;
XX XX
XX DR WPI: 2003-093137/08.
XX DR N-PSDB; ABX56007.
XX DR
XX XX
XX PT New human G-protein coupled receptor HGPRBMY11 polypeptide or
XX PT polynucleotide, useful for preventing, treating or ameliorating e.g.
XX PT myocardial infarction, angina, thrombosis, Alzheimer's disease,
XX PT schizophrenia, AIDS, leukemia
XX XX
XX PS Claim 11; Fig 1; 444pp; English.
XX
XX CC The invention relates to an isolated polypeptide (designated HGPRBMY11),
XX CC which has a G-protein coupled receptor (GPCR) activity (also known
XX CC as GPCR74 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit
XX CC Number PTA-2766, its variants (HGPRBMY11v1 and HGPRBMY11v2), fragments,
XX CC domains, species homologues and proteins 95% similar to it. Also included
XX CC are: (1) the nucleic acids encoding the HGPRBMY11 proteins (including
XX CC variants, fragments, complements and sequences 95% similar to the
XX CC HGPRBMY11 nucleic acids); (2) recombinant vectors; (3) transformed host
XX CC cells expressing HGPRBMY11; (4) an anti-HGPRBMY11 antibody; (5)
XX CC diagnosing a pathological condition or a susceptibility to a pathological
XX CC condition in a subject; (6) identifying a binding partner to the
XX CC HGPRBMY11 polypeptide; (7) identifying an activity in a biological assay;
XX CC (8) a process for making polynucleotide sequences encoding a gene product
XX CC having altered GPCR activity; (9) a shuffled polynucleotide produced by
XX CC the method of (8); and (10) screening for candidate compounds capable of
XX CC binding to and/or modulating activity of a GPCR. The polypeptide or the
XX CC polynucleotide is useful for preventing, treating or ameliorating a
XX CC medical condition, particularly cardiovascular diseases or disorders,
XX CC e.g. myocardial infarction, congestive heart failure, arrhythmias,
XX CC cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina,
XX CC thrombosis or hypertension). The HGPRBMY11 polypeptide or polynucleotide
XX CC is also useful for treating, preventing or ameliorating e.g. Alzheimer's
XX CC disease, Parkinson's disease, osteoporosis, obesity, human
XX CC immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness,
XX CC acquired immunodeficiency syndrome (AIDS), leukemia, sepsis,
XX CC inflammations, psoriasis, Gaucher's disease or ischaemia (many
XX CC other diseases and disorders are listed in the specification).
XX CC The present sequence represents an HGPRBMY11 protein (or variant).
XX
XX Sequence 330 AA;

```

Query Match		100.08; Score 1712; DB 24; Length 330;
Best Local Similarity		100.08; Pred. No. 5.4e-177;
Matches 330; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MEPNGTFSNNNSRNCITENFKREFPIVYLIIFFWGLGSLIYVFLQPKKSTSVNVF 60
Db	1	MEPNGTFSNNNSRNCITENFKREFPIVYLIIFFWGLGSLIYVFLQPKKSTSVNVF 60
QY	61	MLNLAIISDLLFTSTLPPFRADYILRGSNWIFGDLACRIMSYSLYNYMYSIIYFTVLVSVR 120
Db	61	MLNLAIISDLLFTSTLPPFRADYILRGSNWIFGDLACRIMSYSLYNYMYSIIYFTVLVSVR 120
QY	121	FLAWHPFLLHVTIRSANWLOGIITWILMASSIMLDSGSEQSGVTSCLNLKYIA 180
Db	121	FLAWHPFLLHVTIRSANWLOGIITWILMASSIMLDSGSEQSGVTSCLNLKYIA 180
QY	181	KLOTMYIALVVGCLLPFFLTICYLIIIRVLKVEVPSGLRVSHRKALTTIIITLIIF 240
Db	181	KLOTMYIALVVGCLLPFFLTICYLIIIRVLKVEVPSGLRVSHRKALTTIIITLIIF 240
QY	241	FLCFLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACFNPLLYFAGENFKDL 300
Db	241	FLCFLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACFNPLLYFAGENFKDL 300
QY	301	KSALRKGHPQAKTKCVFPVSVWLKRETRV 330
Db	301	KSALRKGHPQAKTKCVFPVSVWLKRETRV 330
RESULT 3		
AAE07539		
ID	AAE07539	standard; Protein: 341 AA.
XX	AAE07539;	
AC	AAE07539;	
XX	AAE07539;	
DT	06-NOV-2001	(first entry)
XX	06-NOV-2001	(first entry)
DE	Human G-protein coupled receptor 1b (GPCR1b) variant.	
XX	Human G-protein coupled receptor; GPCR1b; GPCR1b; cardiomyopathy;	
KW	atherosclerosis; hypertension; congenital heart defect; anorexia;	
KW	atrial septal defect; ventricular septal defect; valve disease;	
KW	scleroderma; obesity; transplantation; adrenoleucodystrophy; AIDS;	
KW	congenital adrenal hyperplasia; prostate cancer; lymphoma; cancer;	
KW	haemophilia; idiopathic thrombocytopenic purpura; dyslipidaemia;	
KW	acquired immune deficiency syndrome; diabetes; infectious disease;	
KW	metabolic syndrome X; Albright Hereditary Osteodystrophy; ASD; VSD;	
KW	neurodegenerative disorder; Alzheimer's disease; immune disorder;	
KW	fertility; Parkinson's disorder; haematopoietic disorder;	
XX	chromosome 13.	
OS	Homo sapiens.	
XX	Homo sapiens.	
PH	Key	Location/Qualifiers
FT	Peptide	1..54
FT	/label= Signal_peptide	
FT	Protein	55..341
FT	/label= Mature_human_GPCR1b_protein_variant	
XX	W0200159113-A2.	
PN	16-AUG-2001.	
XX	16-AUG-2001.	
PD	08-FEB-2001; 2001WO-US04404.	
XX	08-FEB-2001; 2001WO-US04404.	
PR	08-FEB-2000; 2000US-0180929.	
PR	08-FEB-2000; 2000US-0181045.	
PR	09-FEB-2000; 2000US-0181157.	
PR	09-FEB-2000; 2000US-0181339.	
PR	09-FEB-2000; 2000US-0181344.	
PR	09-FEB-2000; 2000US-0183392.	
PR	17-FEB-2000; 2000US-0183191.	
PR	20-JUL-2000; 2000US-0219585.	

PR	20-JUL-2000; 2000US-0219758.	
PR	26-JUL-2000; 2000US-0221341.	
XX	(CURA-) CURAGEN CORP.	
PA	(CURA-) CURAGEN CORP.	
XX	Taupier RJ, Burgess CE, Padigaru M, Tchervet VT, Mishra VS;	
PI	Casman S, Ballinger R, Vernet CAM, Li L, Spytek KA, Andrew DP;	
PI	Mezes PS;	
XX	WPI: 2001-497077/54.	
DR	N-PSDB; RAD13709.	
DR	N-PSDB; RAD13709.	
XX	Novel G-protein coupled receptor proteins (GPCR1-GPCR-7) useful for	
PT	treating or preventing, e.g., cardiomyopathy, atherosclerosis,	
PT	hypertension, acquired immune deficiency syndrome, bronchial asthma,	
PT	Crohn's disease, and multiple sclerosis -	
XX	Claim 1; Page 6; 135pp; English.	
PS	Claim 1; Page 6; 135pp; English.	
XX	The invention relates to human G-protein coupled receptor proteins 1-7	
CC	(GPCR1-7 or GPCR) and nucleic acid molecules encoding such proteins.	
CC	GPCRX sequences are used to treat or prevent a human suffering	
CC	from GPCR-associated disorders, e.g. cardiomyopathy, atherosclerosis,	
CC	hypertension, congenital heart defects, aortic stenosis, atrial septal	
CC	defect (ASD), atrioventricular (A-V) canal defect, ductus arteriosus,	
CC	pulmonary stenosis, subaortic stenosis, ventricular septal defect	
CC	(VSD), valve diseases, tuberculous sclerosis, scleroderma, obesity,	
CC	transplantation, adrenoleucodystrophy, congenital adrenal hyperplasia,	
CC	prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer,	
CC	fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic	
CC	purpura, graft versus host disease, acquired immune deficiency syndrome	
CC	(AIDS), bronchial asthma, Crohn's disease, multiple sclerosis and	
CC	treatment of Albrit Hereditary Osteodystrophy. GPCR antibodies are	
CC	used to treat a pathological state and treat or prevent disorders	
CC	such as diabetes, metabolic disturbances associated with obesity,	
CC	metabolic syndrome X, anorexia, wasting disorders associated with	
CC	chronic diseases, infectious disease, cancer-associated cachexia,	
CC	cancer, neurodegenerative disorders, Alzheimer's disease, Parkinson's	
CC	disorder, immune disorders, haematopoietic disorders and various	
CC	dyslipidaemias. GPCR DNA is also useful in gene therapy. The present	
CC	sequence is human GPCR1b protein variant. The GPCR1 DNA is located on	
CC	chromosome 13.	
XX	Sequence 341 AA;	
SQ	Sequence 341 AA;	
Query Match		100.08; Score 1712; DB 22; Length 341;
Best Local Similarity		100.08; Pred. No. 5.7e-177;
Matches 330; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MEPNGTFSNNNSRNCITENFKREFPIVYLIIFFWGLGSLIYVFLQPKKSTSVNVF 60
Db	12	MEPNGTFSNNNSRNCITENFKREFPIVYLIIFFWGLGSLIYVFLQPKKSTSVNVF 71
QY	61	MLNLAIISDLLFTSTLPPFRADYILRGSNWIFGDLACRIMSYSLYNYMYSIIYFTVLVSVR 120
Db	72	MLNLAIISDLLFTSTLPPFRADYILRGSNWIFGDLACRIMSYSLYNYMYSIIYFTVLVSVR 131
QY	121	FLAWHPFLLHVTIRSANWLOGIITWILMASSIMLDSGSEQSGVTSCLNLKYIA 180
Db	132	FLAWHPFLLHVTIRSANWLOGIITWILMASSIMLDSGSEQSGVTSCLNLKYIA 191
QY	181	KLOTMYIALVVGCLLPFFLTICYLIIIRVLKVEVPSGLRVSHRKALTTIIITLIIF 240
Db	192	KLOTMYIALVVGCLLPFFLTICYLIIIRVLKVEVPSGLRVSHRKALTTIIITLIIF 251
QY	241	FLCFLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACFNPLLYFAGENFKDL 300
Db	252	FLCFLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACFNPLLYFAGENFKDL 311
QY	301	KSALRKGHPQAKTKCVFPVSVWLKRETRV 330
Db	312	KSALRKGHPQAKTKCVFPVSVWLKRETRV 341

RESULT 4
 ABU11939
 ID ABU11939 standard; Protein; 341 AA.
 AC ABU11939;
 XX
 XX
 DT 13-FEB-2003 (first entry)
 XX
 DE Human G-protein coupled receptor HGPBMY11v2.
 XX
 XX Human; receptor; HGPBMY11v1; HGPBMY11v2; GPCR81;
 KW G-protein coupled receptor; cardiovascular disease; arrhythmia;
 KW myocardial infarction; congestive heart failure; cardiomyopathy;
 KW atherosclerosis; arteriosclerosis; embolism; angina; thrombosis;
 KW hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis;
 KW obesity; human immunodeficiency virus infection; HIV; schizophrenia;
 KW sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia;
 KW sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.
 XX
 OS Homo sapiens.
 XX
 XX WO20020286123-A2.
 PN
 XX
 PD 31-OCT-2002.
 XX
 XX 16-NOV-2001; 2001WO-US44019.
 XX
 PR 17-NOV-2000; 2000US-249613P.
 PR 21-DEC-2000; 2000US-257611P.
 PR 16-JUL-2001; 2001US-305818P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX
 XX Feder J, Nelson TC, Ramanathan C, Cacace AM, Barber LE;
 PI
 XX
 XX WPI; 2003-093137/08.
 DR N-PSDB; ABX56021.
 XX
 XX New human G-protein coupled receptor HGPBMY11 polypeptide or
 PT polynucleotide, useful for preventing, treating or ameliorating e.g.
 PT myocardial infarction, angina, thrombosis, Alzheimer's disease,
 PT schizophrenia, AIDS, leukemia
 XX
 XX Claim 33; Fig 15; 444pp; English.
 PS
 XX
 XX The invention relates to an isolated polypeptide (designated HGPBMY11),
 CC which has a G-protein coupled receptor (GPCR) activity (also known
 CC as GPCR74 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit
 CC Number FTA-2766, its variants (HGPBMY11v1 and HGPBMY11v2), fragments,
 CC domains, species homologues and proteins 95% similar to it. Also included
 CC are: (1) the nucleic acids encoding the HGPBMY11 proteins (including
 CC variants, fragments, complements and sequences 95% similar to the
 CC HGPBMY11 nucleic acids); (2) recombinant vectors; (3) transformed host
 CC cells expressing HGPBMY11; (4) an anti-HGPBMY11 antibody; (5)
 CC diagnosing a pathological condition or a susceptibility to a pathological
 CC condition in a subject; (6) identifying a binding partner to the
 CC HGPBMY11 polypeptide; (7) identifying an activity in a biological assay;
 CC (8) a process for making polynucleotide sequences encoding a gene product
 CC having altered GPCR activity; (9) a shuffled polynucleotide produced by
 CC the method of (8); and (10) screening for candidate compounds capable of
 CC binding to and/or modulating activity of a GPCR. The polypeptide or the
 CC polynucleotide is useful for preventing, treating or ameliorating a
 CC medical condition, particularly cardiovascular diseases or disorders,
 CC e.g. myocardial infarction, congestive heart failure, arrhythmias,
 CC cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina,
 CC thrombosis or hypertension). The HGPBMY11 polypeptide or polynucleotide
 CC is also useful for treating, preventing or ameliorating e.g. Alzheimer's
 CC disease, Parkinson's disease, osteoporosis, obesity, human
 CC immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness,
 CC acquired immunodeficiency syndrome (AIDS), leukaemia, sepsis,
 CC inflammations, psoriasis, Gaucher's disease or ischaemia (many
 CC other diseases and disorders are listed in the specification).

CC The present sequence represents an HGPBMY11 protein (or variant).
 XX
 SQ Sequence 341 AA;
 Query Match 100.0%; Score 1712; DB 24; Length 341;
 Best Local Similarity 100.0%; Pred. No. 5.7e-177;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEPNGTFSNNNSRNCCTIENFKREFPIVYLIIFFWGLNGLSIYVFLQPKKSTSVNWF 60
 DB 12 MEPNGTFSNNNSRNCCTIENFKREFPIVYLIIFFWGLNGLSIYVFLQPKKSTSVNWF 71
 QY 61 MLNLAISDLLFISTLPFRADYTLRGSNWIFGLACRIMSYSLYVNMYSIYVFLVLSVVR 120
 DB 72 MLNLAISDLLFISTLPFRADYTLRGSNWIFGLACRIMSYSLYVNMYSIYVFLVLSVVR 131
 QY 121 FLAMVHPRLLHVTLSRSNAWILGIIWILINASSIMLDGSEQNGSVTSCLEINLYKTA 180
 DB 132 FLAMVHPRLLHVTLSRSNAWILGIIWILINASSIMLDGSEQNGSVTSCLEINLYKTA 191
 QY 181 KLOTNMYIALVVGCLLPFTTSLICVLLIIRVLKVPESGLRVSHRKALTTIITLIIF 240
 DB 192 KLOTNMYIALVVGCLLPFTTSLICVLLIIRVLKVPESGLRVSHRKALTTIITLIIF 251
 QY 241 FLCFLPYHTLRTVHLFTWKVGLCKDLRHLKALVTITLALAAANACFNPLIYYPAGENFDEL 300
 DB 252 FLCFLPYHTLRTVHLFTWKVGLCKDLRHLKALVTITLALAAANACFNPLIYYPAGENFDEL 311
 QY 301 KSALRKGHPKOKAKTCVFPVSWLKKETRV 330
 DB 312 KSALRKGHPKOKAKTCVFPVSWLKKETRV 341
 RESULT 5
 AAEL12022
 ID AAEL12022 standard; Protein; 346 AA.
 XX
 AC AAEL12022;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human G-protein coupled receptor, GPCR-1.
 XX
 XX Human; G-protein coupled receptor; GPCR; gene therapy;
 KW proteosoma analysis; cell proliferative disorder; arteriosclerosis;
 KW cancer; neurological disorder; Huntington's disease; Parkinson's disease;
 KW cardiovascular disorder; atherosclerosis; congestive heart failure;
 KW gastrointestinal disorder; gastritis; nausea; autoimmune; anaemia;
 KW inflammatory disorder; acquired immunodeficiency syndrome; AIDS;
 KW metabolic disorder; diabetes; obesity; viral infection; drug screening;
 KW chromosomal mapping; cytostatic; immunomodulatory; antiinflammatory;
 KW virucide.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..55
 FT /label= Signal_peptide
 FT Domain 38..61
 FT /label= Transmembrane_domain
 FT Domain 198..221
 FT /label= Transmembrane_domain
 FT Protein 56..346
 FT /note= "Mature human GPCR-1 protein"
 XX
 XX WO200172836-A2.
 XX
 PD 04-OCT-2001.
 XX
 XX 29-MAR-2001; 2001WO-US10436.
 XX
 XX 29-MAR-2000; 2000US-193051P.
 XX
 XX 06-APR-2000; 2000US-195155P.
 PR

PR 20-APR-2000; 2000US-199084P.
PR 28-APR-2000; 2000US-200551P.
PR 05-MAY-2000; 2000US-202278P.
XX (INCY-) INCYTE GENOMICS INC.
XX Policky JL, Tribouley CM, Tang YT, Baughn MR, Graul R, Khan FA;
PI Nguyen DB, Patterson C, Lal P, Au-young J, Yang J, Hafalia A;
PI Walia NK, Das D;
XX WPI; 2001-616472/71.
DR N-PSDB; AAD19577.
XX New human G-protein coupled receptors, useful for treatment and
PT diagnosis of e.g. cell proliferation, also screening for specific
PT modulators, and related nucleic acid -
XX Claim 1; Page 101-102; 11pp; English.
XX The present sequence is a human G-protein coupled receptor, GCRC-1
CC protein. The GCRCs are used for treating or preventing disorders
CC associated with decreased expression of functional GCRC, and for
CC identifying specific agonists and antagonists, also binding agents
CC and modulators. They can also be used for generating specific antibodies
CC and for proteosome analysis. Disorders that can be treated include
CC cell proliferative disorders, e.g., arteriosclerosis and cancer,
CC neurological disorders, e.g., Huntington's disease and Parkinson's
CC disease, cardiovascular disorders, e.g., atherosclerosis and congestive
CC heart failure, gastrointestinal disorders, e.g., gastritis and nausea,
CC autoimmune/inflammatory disorders, e.g., acquired immunodeficiency
CC syndrome (AIDS) and anemia, metabolic disorders, e.g., diabetes and
CC obesity and viral infections. Nucleic acids that encode GCRC are
CC used for identifying agents that alter its expression, for assessing
CC toxicity of test compounds, and as sources of primers and probes for
CC diagnostic detection of GCRC DNA and of therapeutic antisense and
CC ribozyme sequences. They can also be used in gene therapy, for
CC chromosomal mapping, and for recombinant production of GCRC. The
CC antibodies are useful for diagnosis and monitoring of diseases
CC associated with GCRC expression, for detecting and purifying GCRC,
CC and as therapeutic agents and for drug screening.
XX Sequence 346 AA;
SQ Query Match 100.0%; Score 1712; DB 22; Length 346;
Best Local Similarity 100.0%; Pred. No. 5.8e-177;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPNGTFNNNSRCTTENKREFFPIVLIIFPWGVLGSLYVFLQPKKTSVNVF 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||
17 MEPNGTFNNNSRCTTENKREFFPIVLIIFPWGVLGSLYVFLQPKKTSVNVF 76
QY 61 MLNLATSDLLFTSTLPFRADYILRGSNWIFGDLACRIMSYSLYVNMYSSTYFTVLVSVR 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||
77 MLNLATSDLLFTSTLPFRADYILRGSNWIFGDLACRIMSYSLYVNMYSSTYFTVLVSVR 136
QY 121 FLAMVHPRFLLEVTSRSAMILGGIILWILIMASSIMLDSGSENGSWTSCLEFLNLYKTA 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||
137 FLAMVHPRFLLEVTSRSAMILGGIILWILIMASSIMLDSGSENGSWTSCLEFLNLYKTA 196
QY 181 KLOTNMYALVGGCLLPFFILSTCYLLIIRVLVKVEVPESGLRVSHERKALTTIITLIIF 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||
197 KLOTNMYALVGGCLLPFFILSTCYLLIIRVLVKVEVPESGLRVSHERKALTTIITLIIF 256
QY 241 FLCFPIYHPLRTVHLTTHKVGCLCKDRHLKALVITLALAAANACFNPLLYIFAGENFKDRL 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||
257 FLCFPIYHPLRTVHLTTHKVGCLCKDRHLKALVITLALAAANACFNPLLYIFAGENFKDRL 316
QY 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||
317 KSALRGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 6

ARB82852
ID AAB82852 standard; Protein; 346 AA.
XX
AC AAB82852;
XX
DT 12-NOV-2001 (first entry)
XX
DE Human P2Y-like GPCR protein.
XX
KW P2Y-like; G-protein coupled receptor; GPCR; human;
KW cysteinyl leukotriene receptor; cycloL LTD4; bactericide;
KW fungicide; protozoacide; virucide; analgesic; cytostatic; anabolic;
KW antiasthmatic; antiparkinsonian; cardiant; hypertensive;
KW hypotensive; osteopathic; antiulcer; immunosuppressive;
KW antiallergic; antisclerotic; neuroprotective; antipsychotic;
KW therapy; vaccine.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 41..63
FT /label= TM1
FT /note= "transmembrane domain 1"
FT Domain 77..96
FT /label= TM2
FT /note= "transmembrane domain 2"
FT Domain 114..137
FT /label= TM3
FT /note= "transmembrane domain 3"
FT Domain 156..173
FT /label= TM4
FT /note= "transmembrane domain 4"
FT Domain 202..223
FT /label= TM5
FT /note= "transmembrane domain 5"
FT Domain 249..266
FT /label= TM6
FT /note= "transmembrane domain 6"
FT Domain 296..313
FT /label= TM7
FT /note= "transmembrane domain 7"
XX
PN WO200168842-A2.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-EP02785.
XX
PR 14-MAR-2000; 2000US-0189045.
XX
PA (FARB) BAYER AG.
XX
PI Xiao Y;
XX
DR WPI; 2001-565794/63.
DR N-PSDB; AAB26608.
XX
PT Nucleic acids encoding P2Y-like G-protein coupled receptor proteins,
PT useful for preventing diagnosing and treating, e.g. cancer, multiple
PT sclerosis, ulcers, bullmia and asthma -
XX
PS Claim 1(a); Fig 7; 110pp; English.
XX
CC The present sequence is that of a P2Y-like G-protein coupled receptor
CC (GPCR) that has 7 transmembrane regions. Homology searches showed
CC this receptor to be homologous to cysteinyl leukotriene
CC (cycloL LTD4) receptor and P2Y receptors. The invention provides
CC P2Y-like GPCR polypeptides and polynucleotides, expression vectors,
CC host cells, methods for detecting the polynucleotides, methods of
CC screening for agents which regulate or decrease the activity of a
CC P2Y-like GPCR protein, and a pharmaceutical composition comprising
CC an expression vector containing a P2Y-like GPCR polynucleotide
CC or a reagent that modulates a P2Y-like GPCR polypeptide or

Db 197 KLOTMYVIALVVGCLLPFTTLCICVLLIIRVLKVEPESGLRSHRKALTTIIILIF 256
 QY 241 FLCPLPYHTLRTVHLTTWKVGLCKDLRLHKAIVITLALAAANACFNPLLYFAGENFKDRL 300
 Db 257 FLCPLPYHTLRTVHLTTWKVGLCKDLRLHKAIVITLALAAANACFNPLLYFAGENFKDRL 316
 QY 301 KSALRKGHPQAKTKCVFPVSVWLKTRV 330
 Db 317 KSALRKGHPQAKTKCVFPVSVWLKTRV 346

RESULT 8
 AAU04368
 ID AAU04368 standard; Protein; 346 AA.
 XX
 AC AAU04368;
 XX
 DT 23-OCT-2001 (first entry)
 XX
 DE Human G-protein coupled receptor, hRUP14.
 XX
 KW Human; G-protein coupled receptor; GPCR; hRUP14; agonist;
 KW inverse agonist; lung cancer.
 XX
 OS Homo sapiens.
 XX
 PN WC200136471-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000; 2000WO-US31509.
 XX
 PR 17-NOV-1999; 99US-0166088.
 PR 17-NOV-1999; 99US-0166099.
 PR 17-NOV-1999; 99US-0166369.
 PR 23-DEC-1999; 99US-0171900.
 PR 23-DEC-1999; 99US-0171901.
 PR 23-DEC-1999; 99US-0171902.
 PR 11-FEB-2000; 2000US-0181749.
 PR 14-MAR-2000; 2000US-0189258.
 PR 14-MAR-2000; 2000US-0189259.
 PR 10-APR-2000; 2000US-0195898.
 PR 10-APR-2000; 2000US-0195899.
 PR 10-APR-2000; 2000US-0196078.
 PR 28-APR-2000; 2000US-0200419.
 PR 12-MAY-2000; 2000US-0203630.
 PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.
 XX
 PA (AREN-) ARENA PHARM INC.
 XX
 XX Chen R, Dang HT, Lowitz KP;
 XX
 DR WPI; 2001-355616/37.
 DR N-PSDB; AAS07941.
 XX

Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents - Claim 25; Page 100-101; 160pp; English.

The sequence represents a human G-protein coupled receptor (GPCR), hRUP14. The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists having applicability as therapeutic agents for treating diseases related to GPCR, e.g. lung cancer.

CC Non-endogenous version of human GPCRs are also utilized in research settings and in vitro and in vivo system, incorporating GPCRs can be utilized to elucidate and understand the roles these receptors play in the human condition, both normal and diseased.

XX
 SQ Sequence 346 AA;
 Query Match 100.0%; Score 1712; DB 22; Length 346;
 Best Local Similarity 100.0%; Pred. No. 5.8e-177;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPNGTFSNNNSRNCITENFKREFPIVLIIFWCVLGNGLSIYVLOPKKSTSVNYF 60
 Db 17 MEPNGTFSNNNSRNCITENFKREFPIVLIIFWCVLGNGLSIYVLOPKKSTSVNYF 76
 QY 61 MNLAIISDLIFSTLPPFRADYILRGSNWIFGDLACRIMSISLYVNMYSYIFLTVLSVVR 120
 Db 77 MNLAIISDLIFSTLPPFRADYILRGSNWIFGDLACRIMSISLYVNMYSYIFLTVLSVVR 136
 QY 121 FLAMVHFFRLHVTIRSANILCGIWIILIMASSIMLLDSGSEQSGSVTSCEINLYKIA 180
 Db 137 FLAMVHFFRLHVTIRSANILCGIWIILIMASSIMLLDSGSEQSGSVTSCEINLYKIA 196
 QY 181 KLOTMYVIALVVGCLLPFTTLCICVLLIIRVLKVEPESGLRSHRKALTTIIILIF 240
 Db 197 KLOTMYVIALVVGCLLPFTTLCICVLLIIRVLKVEPESGLRSHRKALTTIIILIF 256
 QY 241 FLCPLPYHTLRTVHLTTWKVGLCKDLRLHKAIVITLALAAANACFNPLLYFAGENFKDRL 300
 Db 257 FLCPLPYHTLRTVHLTTWKVGLCKDLRLHKAIVITLALAAANACFNPLLYFAGENFKDRL 316
 QY 301 KSALRKGHPQAKTKCVFPVSVWLKTRV 330
 Db 317 KSALRKGHPQAKTKCVFPVSVWLKTRV 346

RESULT 9
 AAU07294
 ID AAU07294 standard; Protein; 346 AA.
 XX
 AC AAU07294;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Cysteinyl leukotriene receptor HIPHDM0000007.
 XX
 KW Cysteinyl leukotriene receptor; HIPHDM0000007; antiasthmatic; antiHIV;
 KW antiallergic; antiinflammatory; antiarteriosclerotic; antiarrhythmic;
 KW vasotropic; cytostatic; neuroprotective; antirheumatoid; antiarthritic;
 KW immunosuppressive; antipsoriatic; dermatological; antibacterial;
 KW cerebroprotective; antithyroid; asthma; allergic rhinitis; AIDS;
 KW cardiac arrhythmia; myocardial ischaemia; atherosclerosis; heart failure;
 KW rheumatoid arthritis; immune disorder; dermatitis; septic shock; stroke.
 XX
 OS Homo sapiens.
 XX
 XX WO200159105-A1.
 XX
 PD 16-AUG-2001.
 XX
 XX 12-FEB-2001; 2001WO-GB00560.
 XX
 PR 10-FEB-2000; 2000GB-0003079.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 XX
 XX Cousins DJ, Volpe F, Ignar DM;
 XX
 XX WPI; 2001-514666/56.
 XX
 XX N-PSDB; AAS10778.
 XX
 PT Novel cysteinyl leukotriene receptor polypeptide, termed as
 PT HIPHDM0000007 polypeptide, useful for treating cardiovascular diseases,

PT lung diseases, allergic rhinitis, immune deficiency and disorder -
 XX
 PS Claim 1; Page 47-48; 52pp; English.
 XX
 CC The sequence represents the amino acid sequence of cysteinyl leukotriene
 CC receptor polypeptide, termed as HIPHUM000007. The nucleic acid is useful
 CC for identifying a substance that modulates cysteinyl leukotriene receptor
 CC activity. This substance is useful for treating a subject having a
 CC disorder which is responsive to cysteinyl leukotriene receptor
 CC modulation, such as asthma, chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, cardiac arrhythmia, myocardial ischaemia,
 CC atherosclerosis and heart failure. It is also useful in the therapeutic
 CC treatment and/or prophylaxis of disorders such as acquired immune
 CC deficiency syndrome (AIDS), rheumatoid arthritis, multiple sclerosis,
 CC leukaemia, myasthenia gravis, Grave's disease, systemic lupus
 CC erythematosus, inflammatory bowel disease, encephalomyelitis, psoriasis,
 CC atopic dermatitis, septic shock, stroke and ischaemia reperfusion injury.
 CC The antibody to cysteinyl leukotriene receptor is useful for
 CC immunoprecipitation techniques, as tools to further elucidate the
 CC function of HIPHUM000007 or its variant, and as therapeutic agent. The
 CC nucleic acid is useful for identifying mutations in HIPHUM000007 gene
 CC implicated in human disorders, which is in turn useful for diagnosing the
 CC disorder or susceptibility to the disorder and in assessing the
 CC physiology of the disorders. It is also useful in hybridisation studies
 CC to monitor up- or down-regulation of HIPHUM000007 expression.
 XX
 SQ Sequence 346 AA;

Query Match 100.0%; Score 1712; DB 22; Length 346;
 Best Local Similarity 100.0%; Pred. No. 5.8e-177;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEPNGTFNNNSRNCNTIENKREFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNVF 60
 DB 17 MEPNGTFNNNSRNCNTIENKREFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNVF 76
 QY 61 MLNLATSDLLFTSTLPPRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLVLSVVR 120
 DB 77 MLNLATSDLLFTSTLPPRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLVLSVVR 136
 QY 121 FLAWVHPRLLHVTSIRSAWILCGIWIILWASSIMLLDSGSENGSVTSCLELNLYKIA 180
 DB 137 FLAWVHPRLLHVTSIRSAWILCGIWIILWASSIMLLDSGSENGSVTSCLELNLYKIA 196
 QY 181 KLOTMYIALVVGCLLPFTLSICYLIIIRVLKVEVPESGLRVSHRKALTTIITLIIF 240
 DB 197 KLOTMYIALVVGCLLPFTLSICYLIIIRVLKVEVPESGLRVSHRKALTTIITLIIF 256
 QY 241 FLCFLPYHTLRTVHLTTWKVGLCKDLRHKALVITLALAAANACFNPLLYFAGENFKDRL 300
 DB 257 FLCFLPYHTLRTVHLTTWKVGLCKDLRHKALVITLALAAANACFNPLLYFAGENFKDRL 316
 QY 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
 DB 317 KSALRGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 10

AAB73097
 ID AAB73097 standard; Protein; 346 AA.

XX
 AC AAB73097;

XX
 XX 05-JUN-2001 (first entry)

XX
 XX Human LTC4 receptor SEQ ID NO: 2.

XX
 DE Human; peptide leukotriene receptor; LTC4; allergy;
 KW inflammatory disorder.

XX
 OS Homo sapiens.

XX
 PN W0200119986-A1.

XX
 PD 22-MAR-2001.
 XX
 XX 13-SEP-2000; 2000WO-JP06265.
 XX
 PR 14-SEP-1999; 99JP-0259986.
 XX
 XX (YAMA) YAMANOUCHI PHARM CO LTD.
 PA (HELI-) HELIX RES INST.
 XX
 XX Takasaki J, Kamohara M, Matsumoto M, Saito T, Sugimoto T, Ota T;
 PI Isogai T, Nishikawa T, Kawai Y;
 XX WPI; 2001-244800/25.
 DR N-PSDB; AAF81528.
 XX
 XX New leukotriene C4 receptor protein for screening modifiers of ligand
 PT binding activity for treating allergic and inflammatory disorders, such
 PT as ulcerative colitis and asthma
 XX
 PS Claim 1; Page 63-64; 83pp; Japanese.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC novel human, pig and rat leukotriene C4 receptor. These sequences can
 CC be used to screen for substances that can be used in the treatment and
 CC prevention of allergic and inflammatory disorders including dermatitis,
 CC inflammatory bowel disease, ulcerative colitis, asthma and bronchitis.
 CC The present sequence is the human LTC4 receptor.
 XX

SQ Sequence 346 AA;

Query Match 100.0%; Score 1712; DB 22; Length 346;
 Best Local Similarity 100.0%; Pred. No. 5.8e-177;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEPNGTFNNNSRNCNTIENKREFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNVF 60
 DB 17 MEPNGTFNNNSRNCNTIENKREFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNVF 76
 QY 61 MLNLATSDLLFTSTLPPRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLVLSVVR 120
 DB 77 MLNLATSDLLFTSTLPPRADYILRGSNWIFGDLACRIMSYSLYVNMYSIYFLVLSVVR 136
 QY 121 FLAWVHPRLLHVTSIRSAWILCGIWIILWASSIMLLDSGSENGSVTSCLELNLYKIA 180
 DB 137 FLAWVHPRLLHVTSIRSAWILCGIWIILWASSIMLLDSGSENGSVTSCLELNLYKIA 196
 QY 181 KLOTMYIALVVGCLLPFTLSICYLIIIRVLKVEVPESGLRVSHRKALTTIITLIIF 240
 DB 197 KLOTMYIALVVGCLLPFTLSICYLIIIRVLKVEVPESGLRVSHRKALTTIITLIIF 256
 QY 241 FLCFLPYHTLRTVHLTTWKVGLCKDLRHKALVITLALAAANACFNPLLYFAGENFKDRL 300
 DB 257 FLCFLPYHTLRTVHLTTWKVGLCKDLRHKALVITLALAAANACFNPLLYFAGENFKDRL 316
 QY 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
 DB 317 KSALRGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 11

ABP95624
 ID ABP95624 standard; Protein; 346 AA.

XX
 AC ABP95624;

XX
 XX 06-MAR-2003 (first entry)

XX
 XX Human GPCR polypeptide SEQ ID NO 59.

XX
 DE Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
 KW drug development; gustatory; taste; fragrance; receptor.

XX

OS Homo sapiens.
 XX WO200216548-A2.
 XX 28-FEB-2002.
 XX 30-JUL-2001; 2001WO-TB01446.
 XX 04-AUG-2000; 2000JP-0237818.
 XX 13-FEB-2001; 2001JP-0034434.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX Haga T, Takeda S, Mitaku S;
 XX WPI; 2002-304118/34.
 XX N-PSDB; ABZ42898.
 XX Database global search for G protein-coupled receptors, proteins and
 PT encoded genes for studying in vivo signal transduction mechanism and
 PT identifying targets for drug development -
 XX Claim 10; SEQ ID NO 58; 97pp + Sequence Listing; Japanese.
 XX The invention relates to a method for screening G protein-coupled
 CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins
 CC (ABP95596-ABP95942) by extracting open-reading frames containing 6-8
 CC transmembrane domains with 250-1000 amino acid residues to give a gene
 CC homologous with a known GPCR gene. The receptor proteins and encoded
 CC genes are useful for studying in vivo signal transduction mechanism and
 CC identifying targets for drug development e.g. based on olfactory and
 CC gustatory receptors in form of agonists and antagonists by screening
 CC intrinsic and extrinsic ligands as bitter taste inhibitors, taste
 CC enhancers and fragrance improvers.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 346 AA;
 SQ
 Query Match 100.0%; Score 1712; DB 23; Length 346;
 Best Local Similarity 100.0%; Pred. No. 5.8e-177;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEPNGTFSNNRNCTIENFKREFFPIVLLIIFWGLNGLSIYVFLQPKKSTSVNWF 60
 DB 17 MEPNGTFSNNRNCTIENFKREFFPIVLLIIFWGLNGLSIYVFLQPKKSTSVNWF 76
 QY 61 MLNLAISDLLFISTLPRADYILRGSNWFGLDLACRIMSYSLYVNMYSIYFLVLSVVR 120
 DB 77 MLNLAISDLLFISTLPRADYILRGSNWFGLDLACRIMSYSLYVNMYSIYFLVLSVVR 136
 QY 121 FLAMVHPRLLHVTSTRSWILCGIILWILIMASSIMLDGSGFONGSVTSCLENLKYIA 180
 DB 137 FLAMVHPRLLHVTSTRSWILCGIILWILIMASSIMLDGSGFONGSVTSCLENLKYIA 196
 QY 181 KIQTMNTALVVGCLLPFTTSLICVLLIIRVLLKVEVPESGLVSHRKALTTIITLIIF 240
 DB 197 KIQTMNTALVVGCLLPFTTSLICVLLIIRVLLKVEVPESGLVSHRKALTTIITLIIF 256
 QY 241 FLCFLPHTLTHTVLTWKVGLCKDRHLKALVTITLALANACFNPLIYFAGNFKDR 300
 DB 257 FLCFLPHTLTHTVLTWKVGLCKDRHLKALVTITLALANACFNPLIYFAGNFKDR 316
 QY 301 KSAIRKGGHPOKATKCVFVSVYLRKTRV 330
 DB 317 KSAIRKGGHPOKATKCVFVSVYLRKTRV 346
 RESULT 12
 ABG66684
 ID ABG66684 standard; Protein: 346 AA.
 XX

AC ABG66684;
 XX 30-AUG-2002 (first entry)
 XX Human novel polypeptide #19.
 XX Human; inflammatory condition; shock; sepsis; immune response;
 KW cancer; wound healing; central nervous system disease; haematopoiesis;
 KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon;
 KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone;
 KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis;
 KW bone degenerative disorder; periodontal disease; reperfusion injury;
 KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection;
 KW allergic condition; thrombolysis; thrombosis; coagulation disorder;
 KW fungal infection.
 XX Homo sapiens.
 XX WO200244340-A2.
 XX 06-JUN-2002.
 XX 30-NOV-2001; 2001WO-US47004.
 XX 30-NOV-2000; 2000US-0028952.
 XX (HISE-) HYSEQ INC.
 XX Tang YP, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D;
 PI Yamazaki V, Ujwal ML, Drmanac RT;
 XX WPI; 2002-508509/54.
 DR N-PSDB; ABK94908.
 XX Novel nucleic acids and polypeptides for diagnosis, treatment of
 PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
 PT disorders, cancer and promoting wound healing -
 XX Claim 10; Page 582-583; 672pp; English.
 XX The invention relates to human novel polynucleotides and associated
 CC polypeptides. The polynucleotides and polypeptides are useful for
 CC treating inflammatory conditions such as arthritis, nephritis, Crohn's
 CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
 CC and cancer and for promoting wound healing. The sequences are used to
 CC induce the proliferation of neural cells and regeneration of nerve and
 CC brain tissue, and are useful for the treatment of central and peripheral
 CC nervous system diseases and neuropathies, such as Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease and amyotrophic lateral
 CC sclerosis. The sequences are involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
 CC cell disorders and platelet disorders such as thrombocytopenia,
 CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
 CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
 CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
 CC disease. The sequences of the invention are also useful for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, immune deficiencies and disorders
 CC including severe combined immunodeficiency (SCID), bacterial or fungal
 CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia
 CC gravis, allergic conditions such as asthma, thrombolysis or thrombosis
 CC and coagulation disorders. Sequences ABG66666-ABG66758 represent human
 CC novel polypeptides of the invention.
 XX Sequence 346 AA;
 SQ
 Query Match 100.0%; Score 1712; DB 23; Length 346;
 Best Local Similarity 100.0%; Pred. No. 5.8e-177;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEPNGTFSNNRNCTIENFKREFFPIVLLIIFWGLNGLSIYVFLQPKKSTSVNWF 60
 DB 17 MEPNGTFSNNRNCTIENFKREFFPIVLLIIFWGLNGLSIYVFLQPKKSTSVNWF 76


```

|||||
257 FLCFLPYHFLRVHLTTWKVGLCKDLRLHALVITLALAAANACFNPLLYFAGENFKDRL 316
QY 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
|||||
317 KSALRGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 14
AAEI7231
ID AAEI7231 standard; Protein; 346 AA.
XX
AC AAEI7231;
XX
DT 07-MAY-2002 (first entry)
XX
DE Human CysLT2 GPCR (G-protein coupled receptor).
XX
KW Human; CysLT2 GPCR; G-protein coupled receptor; oedema; asthma;
KW immunological disorder; vascular disorder; reproductive disease;
KW cellular metabolism; growth; development; blood; bone homeostasis;
KW inflammation; allergy; angiogenesis; respiratory distress syndrome;
KW Crohn's disease; blood pressure; protein therapy; anti-inflammatory;
KW inflammatory disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..41
FT /label= Extracellular_domain
FT Modified-site 20..22
FT /note= "N-glycosylation site"
FT Modified-site 26..28
FT /note= "N-glycosylation site"
FT Domain 94..115
FT /note= "Extracellular domain between the second and
FT third transmembrane domains"
FT Domain 175..203
FT /note= "Extracellular domain between the fourth and
FT fifth transmembrane domains"
FT Modified-site 181..183
FT /note= "N-glycosylation site"
FT Domain 268..289
FT /note= "Extracellular domain between the sixth and
FT seventh transmembrane domains"
XX
PN WO200192302-A2.
XX
PD 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US16965.
XX
XX 26-MAY-2000; 2000US-207725P.
XX
XX (REG-) REGENERON PHARM INC.
XX
XX Murphy A, Martin J;
XX
XX WPI: 2002-154523/20.
XX
XX N-PSDB; AAD28591.
XX
XX New HUMAN CysLT2 GPCR (G-protein coupled receptor), useful for
XX diagnosing, preventing and treating inflammatory, immunological or
XX vascular disorders, e.g. asthma, allergy, angiogenesis, Crohn's disease
XX or edema.
XX
XX Claim 2: Fig 1A-1C; 58pp; English.
XX
XX The invention relates to human CysLT2 GPCR (G-protein coupled receptor)
XX polypeptide and its corresponding nucleic acid. The human CysLT2 GPCR,
XX antibodies and compositions are useful for treating the human or animal
XX body, or for diagnosing a disease. Human CysLT2 GPCR is useful for
XX diagnosing, preventing and treating inflammatory, immunological,

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CC vascular disorders, reproductive diseases, or diseases related to
CC cellular metabolism, growth, development, blood and bone homeostasis.
CC These disorders or diseases include asthma, inflammation, allergy,
CC angiogenesis, respiratory distress syndrome, Crohn's disease, oedema,
CC high or low blood pressure growth, development, blood and bone
CC homeostasis. Human CysLT2 GPCR is also used in protein therapy. The
CC present sequence is human CysLT2 GPCR protein.
XX
SQ Sequence 346 AA;
Query Match 100.0%; Score 1712; DB 23; Length 346;
Best Local Similarity 100.0%; Pred. No. 5.8e-177;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEPNGTFSNNRNCTIENKREFFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNF 60
Db 17 MEPNGTFSNNRNCTIENKREFFPIVYLIIFFWGLGNGLSIYVFLQPKKSTSVNF 76
QY 61 MNLAIISDLLFTLTPFRADYILRGSNWIFGLACRIMSYSLVNMYSIYFLTVLSVVR 120
Db 77 MNLAIISDLLFTLTPFRADYILRGSNWIFGLACRIMSYSLVNMYSIYFLTVLSVVR 136
QY 121 FLAMVHPPFLHVTIRSAMWILGCIWILIMASSIMLDSGSEONGSVTSCLENLKIA 180
Db 137 FLAMVHPPFLHVTIRSAMWILGCIWILIMASSIMLDSGSEONGSVTSCLENLKIA 196
QY 181 KLOTMNYIALVVGCLLPFFTLSCYLLIIRVLLKVEVPESGLRVSHRKALTIITLIIF 240
Db 197 KLOTMNYIALVVGCLLPFFTLSCYLLIIRVLLKVEVPESGLRVSHRKALTIITLIIF 256
QY 241 FLCFLPYHFLRVHLTTWKVGLCKDLRLHALVITLALAAANACFNPLLYFAGENFKDRL 300
Db 257 FLCFLPYHFLRVHLTTWKVGLCKDLRLHALVITLALAAANACFNPLLYFAGENFKDRL 316
QY 301 KSALRGHPQAKTKCVFPVSVWLKRETRV 330
Db 317 KSALRGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 15
AAG77965
ID AAG77965 standard; Protein; 346 AA.
XX
AC AAG77965;
XX
DT 25-FEB-2002 (first entry)
XX
DE Human G-protein coupled receptor PFT-017*.
XX
KW Human; G-protein coupled receptor; GPCR; PFT-017*; cytostatic;
KW antiallergic; osteopathic; cardiovascular; immunosuppressive; neoplastic;
KW gene therapy; heart disease; gastrointestinal disease; sleep disorder;
KW immunological disorder; pulmonary disorder; infectious disease;
KW myeloproliferative disease; allergic rhinitis; asthma; COPD; obesity;
KW chronic obstructive pulmonary disease; inflammatory bowel disease;
KW diabetes; metabolic disease; neurological disease; urogenital disease;
KW inflammation; cancer; osteoporosis; cardiovascular disease; infection;
KW allergy; respiratory disease; sensory organ disorder; hair loss;
KW immunological disorder; pulmonary disease; neoplastic disease;
KW vasculitic granulomatous disease; dermatology; psychotherapeutic.
XX
OS Homo sapiens.
XX
XX US2001039037-A1.
XX
XX 08-NOV-2001.
XX
XX 05-APR-2001; 2001US-0826791.
XX
XX 05-APR-2000; 2000GB-0008504.
XX
XX 19-APR-2000; 2000US-198367P.
XX
XX (HARL/) HARLAND L.
PA

```

XX
PI Harland L;
XX
DR WPI; 2002-040722/05.
DR N-PSDB; AAH77279.
XX
PT New PFI-017 protein and polynucleotide encoding the protein, useful for
PT diagnosing or treating metabolic diseases, urogenital disease,
PT immunological disorders, infectious diseases, neoplastic or
PT myeloproliferative diseases -
XX
XX Claim 7; Fig 7B; 39pp; English.
XX
PS The sequence represents a novel G-protein coupled receptor (GPCR),
CC PFI-017* of the invention. The PFI-017 has cytostatic, antiallergic,
CC osteopathic, cardiovascular, and immunosuppressive activity. The
CC polynucleotides may have a use in gene therapy. The polynucleotide is
CC useful for treating allergic disorders, an inflammatory disorder, an
CC immunological disorder, a pulmonary disorder, an infectious disease, a
CC neoplastic or myeloproliferative disease, or a heart disease. The
CC allergic disorder is an allergic rhinitis or asthma, the pulmonary
CC disease is COPD, and the inflammatory disorder is inflammatory bowel
CC disease. PFI-017 polynucleotide sequences may be used for the diagnosis
CC of diseases resulting from expression of PFI-017, and to detect and
CC quantify gene expression in conditions, disorders or diseases in which
CC PFI-017 activity may be implicated. The polypeptides are used to produce
CC anti-PFI-017 antibodies to be used diagnostically to detect and quantify
CC PFI-017 levels in disease states. The antibodies, compounds and
CC compositions which can modulate the peptide can be used in treating
CC obesity, diabetes and metabolic disease, neurological disease, urogenital
CC disease, inflammation, cancer, osteoporosis, cardiovascular disease,
CC gastrointestinal disease, infections, allergy and respiratory disease,
CC sensory organ disorders, sleep disorders, hair loss, immunological
CC disorders, pulmonary diseases, infectious diseases, neoplastic and
CC myeloproliferative diseases, vasculitic granulomatous diseases, and heart
CC diseases. These may also be used in dermatology, and psychotherapeutics.
XX
SQ Sequence 346 AA;

Query Match 100.0%; Score 1712; DB 23; Length 346;
Best Local Similarity 100.0%; Pred. No. 5.8e-177;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPNGTFSNNRNCTIENKREFFPIVYLIIFFWGLNGLSIYVFLQPYKKTSVNVF 60
Db |||||
17 MEPNGTFSNNRNCTIENKREFFPIVYLIIFFWGLNGLSIYVFLQPYKKTSVNVF 76

QY 61 MLNLTSDLLFTSLPRADYLRGNSWIFGLACRIMSYSLVYNMYSIYFLTVLSVVR 120
Db |||||
77 MLNLTSDLLFTSLPRADYLRGNSWIFGLACRIMSYSLVYNMYSIYFLTVLSVVR 136

QY 121 FLAVHFFRLHLVTSIRSAWILCGIILWILIMASSIMLDSGSENGSVTSCLLNLYKIA 180
Db |||||
137 FLAVHFFRLHLVTSIRSAWILCGIILWILIMASSIMLDSGSENGSVTSCLLNLYKIA 196

QY 181 KLOTMNYIALVVGCLLPFFTLSCYLLIIIRVILKVEVPESGLRVSHRKALTIITLIIF 240
Db |||||
197 KLOTMNYIALVVGCLLPFFTLSCYLLIIIRVILKVEVPESGLRVSHRKALTIITLIIF 256

QY 241 FLCFLPYHLIRVHTWTKVGLCKDRLHKALVITILALAAACNPNLLYFAGENFKDRL 300
Db |||||
257 FLCFLPYHLIRVHTWTKVGLCKDRLHKALVITILALAAACNPNLLYFAGENFKDRL 316

QY 301 KSALRKGHPQKAKTKCVPVSVWLKRETRV 330
Db |||||
317 KSALRKGHPQKAKTKCVPVSVWLKRETRV 346

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OM protein - protein search, using sw model

Run on: October 8, 2003, 08:26:59 ; Search time 40 Seconds
(without alignments)
793.392 Million cell upd

title: US-09-991-225-2

Perfect score:

Sequence: 1 MEPNGTFSNNNSRNCIENF.....KAKTKCVFPVSVWLRKETRV 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96158682 residues

Total number of hits satisfying chosen parameters: 283308

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 s
```

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Database :      PIR_76:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	467	27.3	362	S33733	G protein-coupled	
2	447	26.1	308	I50241	G protein-coupled	
3	446	26.1	373	JC4737	G protein-coupled	
4	442	25.8	373	JC4162	p2Y receptor - bov	
5	440	25.7	361	B45680	G protein-coupled	
6	436	25.5	344	T09508	intron 17 purinerg	
7	430	25.1	370	JC5549	heptahelical p2Y5-	
8	418.5	24.4	373	A47556	ATP receptor p2u -	
9	416	24.3	342	I53638	platelet-activatin	
10	416	24.3	375	A54946	p-2u nucleotide re	
11	409.5	23.9	342	A40191	platelet-activatin	
12	404.5	23.6	420	I51667	thrombin receptor	
13	404	23.6	341	S63666	platelet activatin	
14	400.5	23.4	397	S66518	proteinase-activat	
15	398	23.2	380	I38435	angiotensin recept	
16	397	23.2	341	A43572	platelet-activatin	
17	394.5	23.0	355	S45177	chemokine (C-C) re	
18	391	22.8	328	I55450	G protein-coupled	
19	390.5	22.8	355	I49339	macrophage inflamm	
20	390	22.8	399	I48705	proteinase activat	
21	387	22.6	371	JC5796	probable chemoattr	
22	382	22.3	371	JC5498	G protein-coupled	
23	378.5	22.1	378	B55735	lymphocyte-specific	
24	378	22.1	355	JC5067	G protein-coupled	
25	376	22.0	356	I49340	MIP-1 alpha recept	
26	373.5	21.8	387	I69202	G protein-coupled	
27	372.5	21.8	363	I57955	somatostatin recep	
28	372.5	21.8	364	JN0763	somatostatin recep	
29	372.5	21.8	378	A55735	G protein-coupled	

ALIGNMENTS

RESULT 1

S33733
G protein-coupled receptor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C:Accession: S33733
R:Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Buri
FEBS Lett. 324, 219-225, 1993
A:Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor
A:Reference number: S33733; MUID:93285340; PMID:8508924
A:Accession: S33733
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <WEB>
A:Cross-references: EMBL:X73268; NID:9395084; PIDN:CAA51716.1; PID:g395085
C:Superfamily: ATP receptor p2u
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	27.38;	Score	467;	DB	2;	Length	362;
Best local Similarity	30.7%;	Prod. No.	1.3e-31;				
Matches	98;	Conservative	112;	Indels	26;	Gaps	7
y	5	GTSSNNNSRNTCI--ENFKREPPPIVYLIIIFWGVGLNGLSIVTLQPKYKSTSVNVEML	62				
		: : : : : : : : : : : : : : : : : : :					
b	21	GNWAGRATTKCSLTKTGQYIPLTVIIVITGFLGNSVALWVNFVHRPWSGISVYMF	80				
		: : : : : : : : : : : : : : : : : : :					
y	63	NLAISDLFIPTLPRADYYLRGNSWIFGDLACRIMSYSIVNMYSSYIFTLVSVVRFL	122				
		: : : : : : : : : : : : : : : : : : :					
b	81	NLAADFLVLTLPALIFYFNKTDWIFGDVWCKLQRFHFVNLVYCSILFLTCISVHRYT	140				
		: : : : : : : : : : : : : : : : : : :					
y	123	ANYHPRLLHVHTSRSAWILCGIITWILIMASSIML---DSGSENGSVTSCLF----	173				
		: : : : : : : : : : : : : : : : : : :					
b	141	GVVHPRLKSLGRKKKNVAYSSVWALVAVYIAPILFYSGTGVRRNKTI-CYTTADEY	199				
		: : : : : : : : : : : : : : : : : : :					
y	174	LNLYKTAKLOTQFNIALVWVGLCPRLPTFLSICVLLIIIVILKVEVPESGLRVSHKALT	233				
		: : : : : : : : : : : : : : : : : : :					
b	200	LRSFYVSMCTVTFMFCI-----PFLVILGCVGLIIVKALVLYKDLNSPLR---RKSYLV	251				
		: : : : : : : : : : : : : : : : : : :					
y	234	IIITLIIFFFCFPLPHTLTIVHL-----TTWKVGLCKLRDKHALVITTLALAAANACFN	287				
		: : : : : : : : : : : : : : : : : : :					
b	252	IIIVLTFVAVSYLPHEVVKMTLNLRALDQTQPMCAFNDKVYATIQVTRGLASLNSCVDPI	311				
		: : : : : : : : : : : : : : : : : : :					
y	288	LYTFAGENFKDLKLSALRK	306				
		: : : : : : : : : : : : : : : : : : :					
b	312	LYFLAGDTFPRRLSRATRK	330				
		: : : : : : : : : : : : : : : : : : :					

RESULT 2

AL3001 2
I50241
G protein-coupled receptor 6H1 - chicken
N: Alternate names: purinoceptor 6H1
C: Species: Gallus gallus (chicken)

A;Molecule type: mRNA
A;Residues: 1-137,139-373 <LSO>
A;Cross-references: EMBL:449205; NID:G9885; PID:CAA9806.1; PID:G98836
C;Comment: This receptor belongs to a family of G protein-coupled receptors. It resp
C;Genetics:

A: Bios references: Q62-077123, Q6ML-001107
 A: Map position: 3pter-3qter
 C: Superfamily: AMP receptor P2u
 C: Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F: 52-77/Domain: transmembrane #status predicted <TM4>
 F: 88-111/Domain: transmembrane #status predicted <TM2>
 F: 124-152/Domain: transmembrane #status predicted <TM3>
 F: 171-191/Domain: transmembrane #status predicted <TM4>
 F: 214-237/Domain: transmembrane #status predicted <TM5>
 F: 261-282/Domain: transmembrane #status predicted <TM6>
 F: 305-328/Domain: transmembrane #status predicted <TM7>

Query Match 26.1%; Score 446; DB 2; Length 373;
 Best Local Similarity 32.1%; Pred. No. 7.5e-30;
 Matches 102; Conservative 79; Mismatches 111; Indels 26; Gaps 10;

QY	235	ITLIIFFCLFPLVHRLRVHLTT---	WKVGLC-	KDRHLKALVTITALAAANACPNLL	288
		: : : : : :	:	: : : : :	
D6	264	IIVLTAVSVIPFHVMKTNLRARLD	FQTPAMCAFNDAVYATYOVRGLASLN	SCVDPII	323
		: : : : : :	:	: : : : :	
QY	289	YVFAGNFKDRLKSALRK		306	
		: : : :			
D6	324	YFLAGDTFRRLSRATR		341	
		: : : :			

```

RESULT 4
JC4162
P21 receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
C:Accession: JC4162
R:Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.

```

Matches	102;	Conservative	63;	Mismatches	135;	Indels	18;	Gaps	7;
QY	3	PNGTFSNNRNCTIENKREFFPIVLIITFIIPWGLNGLSIYVFLQPYKRSSTVNVFML	62						
Db	1								
Db	12	PSATPGQNDCLYAHHSRTAVMPHLSYVFIIGVGNLLALWIVQNRKKNSTTLYST	71						
QY	63	NLAISDLLISVLPRADYIYLEGSNWIFGDLACRIMSYSLYVNMYSIYFVLTVLSVVRFL	122						
Db	1								
Db	72	NLVSIDILFTTALPRYAYAGDFWRIGALCRITAFVYINTYAGVNFCTCUSDIFFI	131						
QY	123	AMVHPFRLHVTISRSWILQGIWILIMASSI-MLLDSGSEQNGSVTSCLEL-NLYKIA	180						
Db	1								
Db	132	AVVHPLRYNKKIRBEHAKGVCIFFWILVFAQTGLPINPMKQERITOMENPFEETK	191						
QY	181	KLOMNYIALVGCGLLPFTTISCYLLIIRVLKVE-----VPESGLRVSRKALTTII	235						
Db	1								
Db	192	SLPWWILGACFIYVLPVLIILICYICCKLFTAKONPLTEKSGV--NKKALNTIIL	248						
QY	236	TLIIFFLCFPHYTLRTVHLATWKVGL-----CKDR--LHKALVTILALAAANACENPLL	288						
Db	1								
Db	249	LIIVFVLCTPYHVALIQHMVK-KLRSENLECSQRHSFQISLHFTVCLMNFNCMDPFI	307						
QY	289	YYPAGENFDRLKSALRK	306						
Db	1								
Db	308	YTFACKGYRKYMRMLKR	325						
RESULT 6									
T09508									
intron 17 purinergic receptor P2Y5 - human									
N/Alternate names: G-protein coupled receptor									
C/Species: Homo sapiens (man)									
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999									
R/Bohm, S. K.; Trumpp, A.; Khitin, L. M.; Kong, W.; Payan, D. G.; Bunnett, N. W.									
submitted to the EMBL Data Library, April 1997									
A/Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the ret									
A/Reference number: Z16705									
A/Accession: T09508									
A/Status: preliminary; translated from GB/EMBL/DBJ									
A/Molecule type: mRNA									
A/Residues: 1-344 <BO>									
A/Cross-references: EMBL:AF000546; NID:g2232068; PID:g2232069									
C/Genetics:									
A/Map position: 13									
C/Superfamily: ATP receptor p2u									
C/Keywords: G protein-coupled receptor; transmembrane protein									
Query Match 25.5%; Score 436; DB 2; Length 344;									
Best Local Similarity 32.0%; Pred. No. 4.7e-29;									
Matches 98; Conservative 73; Mismatches 113; Indels 22; Gaps 8;									
QY	11	NSRRCCTI-ENFKREFFPIVLIIPWGLNGLSIYVFLQPYKRSSTVNVFMLAISDL	69						
Db	1								
Db	5	NSSCFYNDSEFKTYLGOMFSVFIGLVSNCAIYIFICVLKVRNETTYINLAISDL	64						
QY	70	LFISTIFPRADYILRSNWIFGDLACRIMSYSLYVNMYSIYFVLTVLSVVRFLAMVHPR	129						
Db	1								
Db	65	LFVTLTFLRI-FYTTNRNPFGLDLCKISVMLFTYNNMYSIYFVLTVLSVVRFLAMVHPR	123						
QY	130	LLHYTSRRAWILCGIITWILM--ASSIMLLDSGSEQNGSVTSCLELNLKRIKALQTMN	186						
Db	1								
Db	124	SKLTETENAKIVCTGWLTVIGGSAPAVFQSTHSGGNASEACFE-NPEEATWKYLS	182						
QY	187	YIAL---VWGCLLPFTTISCYLLIIRVLKVEVPESGLRVSRKALTTIITIIIFPLC	243						
Db	1								
Db	183	RIVTIFIEIVGFFPIILINVTGSSMWLKLTKR-PVTLRSRKINKTKVLMKMFVHLTIIFCFC	241						
QY	244	FLPHTLTFTVHLTWKVGKCDRLHKALV-----ITLALAAANACENPLLYFVAGEN	295						
Db	1								
Db	242	FPVFN----INLLYSLVETQTFVNCVAAVTRMPTILCIAVSNCCDFPIYFTTSDT	297						
QY	296	FKDLRK	301						

```

Db      298 IONSIK 303
      :: :|
RESULT 7
JC5549
heptahelical P2Y5-like receptor - human
C:Species: Homo sapiens (man)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 24-Sep-1999
C:Accession: JC5549
R:Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A:Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.
A:Reference number: JC5549; MUID:97366605; PMID:9223435
A:Accession: JC5549
A:Molecule type: DNA
A:Residues: 1-370 <MAN>
A:Cross-references: DBJ:AF005419; NID:g2240034; PIDN:AA866322.1; PID:g2240035
C:Superfamily: ATP receptor P2u

      Query Match      25.18; Score 430; DB 2; Length 370;
      Best Local Similarity 31.78; Pred. No. 1.6e-28;
      Matches 103; Conservative 70; Mismatches 132; Indels 20; Gaps 9;

Qy      5  GTFSSNNRNCTI-ENFKREFPPIYVLIIFFWGLGSLIYVFLQPKKSTSVNFMNLN 63
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      23  GNATANNT--CIVDSEKYNLNGAVSVVFLGLITNSVLSLFCFMRMRSETAIFTN 80
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      64  LAISDLLISLTPFRADYILRGSNWIFGDLACRIMSYSLVNMYSYIPLTVLSVVRFLA 123
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      81  LAVSDLLFVCLPFI-KI-FYNFNHWPFGDTLCKISGTAFTNIYGSMLFLTCISVDRELA 139
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      124  MVHPFLRLVTSIRSAWILGCIWILIMASSIML--LDGSGQSGSVTSCLNLYKIAK- 181
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      140  IVPPRSRTIRNSAIVCAGVWILVLSGGSASLSFTTNWNAATTCTCEGLSKRWKT 199
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      182  -LOTNMYALVVGCLLPFFLSICYLIIIRVLKVEPESGLRSHRKALTIITLIIF 240
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      200  YLSKTIFFVYVLIILINLVSCSVLRLTK--PATLSQIGTNKKKVKLMITVHMVAF 258
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      241  FLCFLPYHTLVHTTWKVGCK--DRLHKALY-ITLALAAANACFNPLIYYPAGDNF 296
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      259  VVCFYPSVLFVALYRSQAITNCFLEFAKIMYPITLCIATLNCCFPFIYITLESF 318
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      297  KD-----RLKSALKRGHPQAK 313
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      319  QKSYFINAHIRWESLFTETPLTK 343
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 8
A47556
ATP receptor P2u - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Accession: A47556
R:Lustig, K.D.; Shlauer, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A:Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
A:Reference number: A47556; MUID:93281707; PMID:7685114
A:Accession: A47556
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373 <JUS>
A:Cross-references: GB:L44751; NID:g309457; PIDN:AAA39871.1; PID:g309458
C:Superfamily: ATP receptor P2u
C:Keywords: transmembrane protein

      Query Match      24.4%; Score 418.5; DB 2; Length 373;
      Best Local Similarity 31.8%; Pred. No. 1.5e-27;
      Matches 106; Conservative 67; Mismatches 131; Indels 29; Gaps 10;

Qy      1  MEP-----NGTFSSNN--SRNCTI-ENFKREFPIYVLIIFFWGLGSLIYVFLQPKK 53
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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Db      5  LEPWNSITNGDDELGYKCRFNEDFYVLLPVSYGVGVCLGLNVAIYIFLCRLKT 64
Qy      54  STSVNFMNLALISDLFIETLPPRADYILRGSNWIFGDLACRIMSYSLVNMYSYIPL 113
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      65  WNASITMEHLAVSDSLYAAASPLLVYVYARGDHPPEFVLCVRLFYFNLVCSILFL 124
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      114  TVLSVVRFLAWHPFRLHVTIRSANTILGCIWILIMASSIML-----DSGSEONGS 167
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      125  TCISVHRCGLVRLPLSLRWGRARYAAVAVVWLVLACQAPVLYFVTTSVRGTRITCH 184
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      168  VTSCLNLYKIAKLOTMNYIALVVGCL--LPFFISICVLIIRVLKVEV-PESGLRV 224
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      185  DTSARELFSHVA-----YSSWMLGLLFAVFPFVSVILVCMARLLKPAYCTGGLPR 238
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      225  SHRKALVTIITLIIFFLPFLPYHTLRVHTTWKVGCL-CK--DRLHKALYITLALAAAN 281
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      239  AKRKSVRTIALVLAVALFCFLPFHVTRTLYYSFSDLSLCHTINAINMAYKITRPLASAN 298
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      282  ACENFLIYFAGENFKDRLSALKRGHPQAKT 314
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      299  SCLDFVLYFLAGQ-----RLVRFARDAKPPTEPT 327
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 9
SI3638
platelet-activating factor receptor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999
C:Accession: SI3638
R:Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.,
Nature 349, 342-346, 1991
A:Title: Cloning by functional expression of platelet-activating factor receptor from
A:Reference number: SI3638; MUID:91101726; PMID:1846231
A:Accession: SI3638
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-342 <HON>
A:Cross-references: GB:X56736; NID:g49442; PIDN:CAA40060.1; PID:g49443
A:Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, relea
C:Superfamily: ATP receptor P2u

      Query Match      24.3%; Score 416; DB 2; Length 342;
      Best Local Similarity 30.4%; Pred. No. 2.2e-27;
      Matches 97; Conservative 67; Mismatches 137; Indels 18; Gaps 7;

Qy      11  NSRNCITENFKREFPIYVLIIFFWGLGSLIYV--LOPYTKKSTSVNFMNLALISD 68
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      4  NSSRVDSEFRYTLFPIYVLIIFVLIITANGYVLMWFAFLYPSKLINEIKIFMVLAVD 63
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      69  LLIETLPPRADYILRGSNWIFGDLACRIMSYSLVNMYSYIPLTVLSVVRFLAWHPF 128
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      64  LLFLITPLIIVYISNOGWNFLPKFLCMLAGCLFFINTYCSVAFGLVITYNRFOAVKPI 123
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      129  RLLHVTIRSANTILGCIWILIM--ASSIMLLD-----SGSEONGSVTSCLNLYKIAK 181
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      124  KTAQATTRKRGIALSLVINVAIVAAASFLVMDSTNVVSKAGSGNITRCFE-HVKGSK 182
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      182  LOTMNYIALVVGCLLPFFLSICYLIIIRVLKVEPESGLRSHRKALTIITLIIFP 241
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      183  PVLIIHICIVLGFPIVFLIILFCNLVIITLTLQVFKQQRNAAEVRRLAAVAVCVLAVF 242
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      242  LCLFPHYHTLVHTTWKVGCLCKDLHKAL---VITLALAAANACFNPLIYYPAGNFK 297
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      243  ICFVPHHMQV-LFWTLAELOMPSSNNHQAINDAHOVTLCLLSTNCVLDPVICYCLTKKR 301
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy      298  DRKSALKRGHPQAKTKC 316
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      302  KHLSEKL---NIMRSEKQC 317
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 10
A54946
P-2U nucleotide receptor - human

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J. Biol. Chem. 266, 20400-20405, 1991

A:Title: Molecular cloning and expression of platelet-activating factor receptor 1
A:Reference number: A41079; PMID:92041873; PMID:1657923

A:Accession: A41079

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-342 <NAK>

A:Cross-references: GB:D10202; GB:D90433; NID:g219875; PIDN:BA01050.1; PID:g219976

R:Sugimoto, T.; Tsuchimoto, H.; Mcgregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, T. Biochem. Biophys. Res. Commun. 189, 617-624, 1992

A:Title: Molecular cloning and characterization of the platelet-activating factor receptor

A:Reference number: J01359; PMID:93112021; PMID:1281995

A:Accession: J01359

A:Molecule type: mRNA

A:Residues: 1-315, 'N', 317-342 <UG>

A:Experimental source: heart

A:Note: the authors translated the codon AAT for residue 316 as Lys

R:Sevriy, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W. Genomics 13, 832-834, 1992

A:Title: The human platelet-activating factor receptor gene

A:Reference number: A42831; PMID:92347886; PMID:1322356

A:Accession: A42831

A:Molecule type: DNA

A:Residues: 1-226, 'TG', 229-342 <SEY>

A:Cross-references: GB:M88177; NID:g190697; PIDN:AAA60214.1; PID:g190698

A:Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBITP:109814)

R:Chase, P.B.; Halonen, M.; Regan, J.W. Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993

A:Title: Cloning of a human platelet-activating factor receptor gene

A:Reference number: J51923; PMID:93192035; PMID:8383507

A:Accession: J51923

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-342 <RES>

A:Cross-references: GB:556396; NID:q298580; PIDN:AAB25755.1; PID:q298581

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QY 288 LIYFAGENPKDLKSLARKGHPQAKTKC 316
      :| | :| | :| | :| | :| |
Db 292 IYCFUTKKR---KHLTKFYMSRRSKC 317
      :| | :| | :| | :| | :| |

RESULT 12
IS1667
thrombin receptor - African clawed frog
C:Species: xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: IS1667
R:Gerstzen, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevich, T.; Turck, C.W.; Vu, T.H.; O'
Nature 368, 648-651, 1994
A:Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac
A:Reference number: IS1667; MUID:94195429; PMID:8145852
A:Accession: IS1667
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-420 <GER>
A:Cross-references: EMBL:U09632; NID:g495197; PIDN:AAA18498.1; PID:g495198

Query Match 23.6%; Score 404.5; DB 2; Length 420;
Best Local Similarity 32.4%; Pred. No. 2.5e-26;
Matches 99; Conservative 61; Mismatches 123; Indels 23; Gaps 6;

QY 13 RNCITP-----NFKREFPIVYLIIFWGLNGLSIVFLQPKYKSTSVNFMNLIA 65
      ||||| :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 85 RNITAEQYLSSQWLAKFVPSLYTVFVGLPLNLLAIIFLKKVKRPVAVYMLIA 144
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 66 ISDLFISTLPADRYLRSNIFGDLACRIMSYSLVNNYSIYFLVLSVWFLAW 125
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 145 IADVFFSVLPFKAYHLSGNDWLFPGMCRIVAFYFCNNYCVLLIASISVDVFLAV 204
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 126 HPPRLHVTSTRSAMILCGIITWILINASSIMLLDSGEQ---NGSVTSCLNLYKIAKL 182
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 205 YMHSLSWRTMSRATMACSTWLSIASTIPLLVETQFKIPRLDITDCHVDVLDKLDK 264
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 183 QTNVNYALVVGCLL----PFTLSICYLIIIRVLKVEPESGLRVSHRKALTITIIILI 238
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 265 FYIYFSSP--CLLFFVFPFIITTCYIGIIRSLSSSSIENS---CKKTRALFLAVVYLC 319
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 239 IFPLCPYHTLTHTVTKVGLCKDLRLKALVTTLALAAANACFNPLLYFYACENFKD 298
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 320 VFIIICGPNVFLFTHY----LQANEFLYEAYILISACVGSVSCCLDPLIYVYASSQQR 375
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

QY 299 RLKSL 304
      :| |
Db 376 YLYSL 381

RESULT 13
S6366
platelet activating factor receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S6366
R:Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.
Biochem. J. 314, 671-678, 1996
A:Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localiz
A:Reference number: S6366; MUID:96239129; PMID:8670084
A:Accession: S6366
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-341 <ISH>
A:Cross-references: EMBL:D50872; NID:g1256924; PIDN:BA09468.1; PID:g1256925
C:Superfamily: ATP receptor P2u

Query Match 23.6%; Score 404; DB 2; Length 341;
Best Local Similarity 30.5%; Pred. No. 2.2e-26;
Matches 101; Conservative 66; Mismatches 134; Indels 30; Gaps 10;

QY 1 MERNFTSNNSRNTCTENFKREFPIVYLIIFWGLNGLSIYF--LQPKYKSTSVN 58
      ||||| :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

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Db 1 MEHNGSRVDS-----EFYTLFPIVYSVILGTVANGVYLVWVFANLPSPKLNLEIK 53
QY 59 VFMNLALISDLLEFISTLPADRYLRSNIFGDLACRIMSYSLVNNYSIYFLVLSV 118
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 54 IFMVLNLMADLLFLITPLVIIVYNEGDWILFNFCNVAGCLFFINTYCSVAFGLVITY 113
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
QY 119 VRELAMVHPFRLHVTSTRSAMILCGIITWILINASSIMLLDSGS-----EONGSVTSC 171
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 114 NRYQAVYPIKTAQATRRKRGISLSLIWISVATSYLATDSNLVFNKDGSGNITRC 173
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
QY 172 LE-LNLYKIAKLOTMYIALVVGCC-LLPFFTLSCYLLIIRVLKVEPESGLRVSHRKA 229
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 174 FEHTEPISVILVVHVFIAF---CFELVFELIFVCLNVIHLLTQPMRQQRKAGVKRRA 230
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
QY 230 LTTIILIIIFFLCPFLPYHTLTFTVHTLTKVGLCKDLKHAL---VITLALAAANACN 285
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 231 LNMVCTVLAIVFIICFVPEHVQ--LPWTIAELGY-QTNFQAIINDAHQITICLLSTNCVLID 288
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
QY 286 PLLIYFAGENFKDLKSLARKGHPQAKTKC 316
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 289 PVIYCFELTKFKRKLS---EKFYSMRSTRKC 316
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |

RESULT 14
S66518
proteinase-activated receptor 2 precursor - human
C:Species: Homo sapiens (man)
C>Date: 28-Oct-1996 sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C:Accession: S66518; S64709; G02131
R:Nystedt, S.; Emilsson, K.; Larsson, A.K.; Strombeck, B.; Sundelin, J.
Eur. J. Biochem. 232, 84-89, 1995
A:Title: Molecular cloning and functional expression of the gene encoding the human F
A:Reference number: S66518; MUID:96048032; PMID:7556175
A:Accession: S66518
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <NYS>
A:Cross-references: EMBL:Z49993; NID:g1008084; PIDN:CAA90290.1; PID:g1008085
Biochem. J. 314, 1009-1016, 1996
A:Title: Molecular cloning, expression and potential functions of the human proteinase
A:Reference number: S64709; MUID:96177879; PMID:8615752
A:Accession: S64709
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137, 'A', 139-397 <BOE>
A:Cross-references: EMBL:U34038; NID:g1041728; PIDN:AAB47871.1; PID:g1041729
R:Kahn, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
A:Reference number: H00822
A:Accession: G02131
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 29-397 <RAH>
A:Cross-references: EMBL:U36753; NID:g1208539; PIDN:AAA90957.1; PID:g1208540
C:Genetics:
A:Map Position: 5q13
A:Introns: 28/1
C:Superfamily: ATP receptor P2u
F:1-36/Domain: activation peptide #status predicted <APT>
F:1-25/Domain: signal sequence #status predicted <SIG>
F:37-397/Product: proteinase-activated receptor 2 #status predicted <MAT>

Query Match 23.4%; Score 400.5; DB 2; Length 397;
Best Local Similarity 30.7%; Pred. No. 5.1e-26;
Matches 99; Conservative 69; Mismatches 121; Indels 33; Gaps 9;

QY 24 EPIYVLIIFWGLNGLSIVFLQPKYKSTSVNFMNLALISDLFISTLPADRYL 83
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
Db 77 FLPITVITVIVVGLPSNGMALWFLFRKKKHPAVIYMANLALADLESIWFPDKIAIHI 136
      :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
QY 84 RGSNWFGLDLACRIMSYSLVNNYSIYFLVLSVWFLAMVHPFRLHVTSTRSAMILC 143

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Db      137 HGNNWYIGALCNVLGFFYGNMYCSILEMCLCSYQRYWTVVPMG-----HSRKKANIAI 192
QY      144 GI---TWILIMASSTML-----LDSGSEQNGSVTSCLELNLYKIATKLQTMNY-I 188
Db      193 GISALWLLILVTLPLVVKQIFIPAL-----NITVCHVILPEQLVGDWFMNPL 244
QY      189 ALVVGCLLPFFTLISYCLIIIRVLLKVEVPESGRVSRKALTTIITLIIFFLCFLPY 247
Db      245 SLAIGVFLPAPLTAFAVLMIRMRSSAMENSEK-KRKRAIKLIVTVLAWVLICFTPS 303
QY      248 HTLRTVHLTWXVGLCKDRHLKALVITLALAAANACFNPLYPAGENFKDRKLSALRKG 307
Db      304 NLLVYHYFLIK-SQGSHVYALYVALCLSTLNSCIDPFYIYFVSHDFDHAKNALL-- 360
QY      308 HPQAKTKCVFPVSVWLKTR 329
Db      361 -CRSVTVKQMVSLTSKKHSR 381

RESULT 15
I38435
angiotensin receptor homolog APJ - human
C:Species: Homo sapiens (man)
C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 21-Jul-2000
C:Accession: I38435
R:O'Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petr
Gene 136, 355-360, 1993
A:Title: A human gene that shows identity with the gene encoding the angiotensin recept
A:Reference number: I38435; MUID:94124031; PMID:8294032
A:Accession: I38435
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <RES>
A:Cross-references: EMBL:U03642; NID:g425351; PIDN:AAA18954.1; PID:g245352
C:Genetics:
A:Gene: APJ
A:Map position: 11q12
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin

Query Match      23.2%; Score 398; DB 2; Length 380;
Best Local Similarity 29.2%; Pred. No. 7.8e-26;
Matches 100; Conservative 71; Mismatches 134; Indels 38; Gaps 13;
QY      1 MEENGFESN----NNSRNCITENKRE--FFPIVYLIIFFWGLNGLSIY-VFLQPKK 53
Db      1 MEEGGDFDNYGADNQSECYTDWKSGLIPAIYMLVFLGTTGNGLVLTWTVFRSSREK 60
QY      54 STSVNFMNLALISDLFIPTLPFRADYILRGSNWIFGDLACRIMSYSLXVNNYSIYFL 113
Db      61 RRSADIFIASLAVADLTFWVPLWATYTYRDYDFGTFGFKLSVLIIEVNNYASVFL 120
QY      114 TVLSVVRFLAMVHPPELLVHTSIRSANILCGIILWIL--IMASSIMLL-DSGSEQNGSVTS 170
Db      121 TGLSFDYRLAIYRVPANARLRLVSGAVATAVLWLAALLAMPVWVLTGTDLENITKVQ 180
QY      171 CLELNLYKIATKLQ-----MNYIALVWGLCPFTTISICYLIIIRVLL-----KVEV 217
Db      181 CY-MDYSMVATVSSWEANEVGLVSSVTGVPVFTIMLTCTYFCTAGTGHFKERIE- 238
QY      218 PESGLRVSRKALTTIITLIIFFLCFLPYHLTRVH-----LTTWKVGLCKDRHLKALVI 273
Db      239 ---GLR-KRRRLSIIIVLVVTFALCWMPYHLVKTLYMLGSLLEWP---CDFDLFLMNIF 291
QY      274 --TLAALAAACENPLLYFAGENKDRKLSALRKGHPQAKT 314
Db      292 PYCTISYVNSCLNPLFAFFDPFRQACTSMICCGSRCACT 334
```

Search completed: October 8, 2003, 08:28:16
Job time : 42 secs